



SEQUENCE LISTING

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ARNAU, Jose
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<120> MUCOR RECOMBINANT GENE EXPRESSION

<130> WOLFF=3

<140> 10/092,947

<141> 2002-03-08

<150> US 60/274,650

<151> 2001-03-12

<160> 65

<170> PatentIn version 3.2

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1 5 10 15
tac acg cag ctg ttg aca gag tta cat aac gaa tac tgc gct gag caa 637
Tyr Thr Gln Leu Leu Thr Glu Leu His Asn Glu Tyr Cys Ala Glu Gln
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cca cta gat gtg ctt cag ttc tgc tcc aac ttt ttc att cgc aaa ctc 685
Pro Leu Asp Val Leu Gln Phe Cys Ser Asn Phe Phe Ile Arg Lys Leu
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gaa gag cag cgc ttg gag cat aga aac aac cac cat tcc cgtaacaact 734
Glu Glu Gln Arg Leu Glu His Arg Asn Asn His His Ser
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g ccn aat gat acc agt aat gat tta cat cct ttg tgt gag caa cca caa 843
Pro Asn Asp Thr Ser Asn Asp Leu His Pro Leu Cys Glu Gln Pro Gln
65 70 75
gaa gac ttt tca caa cag caa ggc atc cag tgg gaa acc acg cat atg 891
Glu Asp Phe Ser Gln Gln Gln Gly Ile Gln Trp Glu Thr Thr His Met
80 85 90
ggc cat ccc aac gac cac ggt gct ctt cat gat gat gat gat gat ccg 939
Gly His Pro Asn Asp His Gly Ala Leu His Asp Asp Asp Asp Asp Pro
95 100 105
ttg gaa gac gaa gac gat gaa gag ttt gac aaa ttt tca act gaa cct 987
Leu Glu Asp Glu Asp Asp Glu Glu Phe Asp Lys Phe Ser Thr Glu Pro
110 115 120 125
ttg ccc tcg ctg cct ccc aca aac tat aac cgt ggc cgc cgc aca tct 1035
Leu Pro Ser Leu Pro Pro Thr Asn Tyr Asn Arg Gly Arg Arg Thr Ser
130 135 140

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Val Lys Cys Arg Glu His Gly Thr Gln Arg Gln Pro Arg Leu Cys Gln	
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ggg cat cat ccc caa atc tca ggc aca agc gag cgc atc aaa gtc tcc	1131
Gly His His Pro Gln Ile Ser Gly Thr Ser Glu Arg Ile Lys Val Ser	
160 165 170	
atc agc aac aac ttt ttg ttt cgc aac ctg gac gaa gag cag tac ctg	1179
Ile Ser Asn Asn Phe Leu Phe Arg Asn Leu Asp Glu Glu Gln Tyr Leu	
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gat gtg gtg aat gcc atg tct gaa aag cgc gtc gtc aag ggc acc aca	1227
Asp Val Val Asn Ala Met Ser Glu Lys Arg Val Val Lys Gly Thr Thr	
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Gly Thr Leu Asp Cys Phe Ile Gly Gln Asn Lys Val Thr Asn Tyr Glu	
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Ala Ala Thr Ile Ile Thr Thr Ser Asp Ser Val Leu Trp Ala Leu Asp	
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Arg Asn Thr Ser Ala Pro Ser Leu Met Glu Asn Thr Ser Arg Lys Arg	
270 275 280 285	
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Arg Met Tyr Glu Tyr Phe Leu Ser Glu Val Val Leu Leu Lys Ser Leu	
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Glu Ser Tyr Glu Gln His Lys Ile Ala Asp Ala Leu Glu Ser Val Tyr	
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Phe Glu Asp Gly Gln Glu Val Val Lys Gln Gly Asp Val Gly Asp Gln	
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Phe Tyr Ile Ile Glu Ser Gly Glu Ala Ile Val Leu Lys Glu Glu Asn	
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ctg gcc ctg tta aac gat gct cct cga gct gca acc gta gtt gct cac 1811
Leu Ala Leu Leu Asn Asp Ala Pro Arg Ala Ala Thr Val Val Ala His
370 375 380

ggc aga ctc aag tgc gct aca ctg ggc aaa aag gca ttc act cgt ctt 1859
Gly Arg Leu Lys Cys Ala Thr Leu Gly Lys Lys Ala Phe Thr Arg Leu
385 390 395

ctt ggc cct gtt ttg gac atc ttg aag cgt aat tca gaa aac tat cat 1907
Leu Gly Pro Val Leu Asp Ile Leu Lys Arg Asn Ser Glu Asn Tyr His
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Ala Val Ile Asn Gln Gln Ser
415 420

aaataaaaaac catggatact ttccgatctg atgttgactt gactgtaaca aagcgacagg 2018

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atggcgccaa tttcaccatc atggtttgtg gtaagacata tgtatacttg caagtgaag 2378

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Pro Leu Asp Val Leu Gln Phe Cys Ser Asn Phe Phe Ile Arg Lys Leu
35 40 45

Glu Glu Gln Arg Leu Glu His Arg Asn Asn His His Ser Pro Asn Asp
 50 55 60

Thr Ser Asn Asp Leu His Pro Leu Cys Glu Gln Pro Gln Glu Asp Phe
 65 70 75 80

Ser Gln Gln Gln Gly Ile Gln Trp Glu Thr Thr His Met Gly His Pro
 85 90 95

Asn Asp His Gly Ala Leu His Asp Asp Asp Asp Asp Pro Leu Glu Asp
 100 105 110

Glu Asp Asp Glu Glu Phe Asp Lys Phe Ser Thr Glu Pro Leu Pro Ser
 115 120 125

Leu Pro Pro Thr Asn Tyr Asn Arg Gly Arg Arg Thr Ser Val Lys Cys
 130 135 140

Arg Glu His Gly Thr Gln Arg Gln Pro Arg Leu Cys Gln Gly His His
 145 150 155 160

Pro Gln Ile Ser Gly Thr Ser Glu Arg Ile Lys Val Ser Ile Ser Asn
 165 170 175

Asn Phe Leu Phe Arg Asn Leu Asp Glu Glu Gln Tyr Leu Asp Val Val
 180 185 190

Asn Ala Met Ser Glu Lys Arg Val Val Lys Gly Thr Thr Val Ile Glu
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Gln Gly Ser Val Gly Asp Phe Phe Tyr Val Val Glu Ser Gly Thr Leu
 210 215 220

Asp Cys Phe Ile Gly Gln Asn Lys Val Thr Asn Tyr Glu Ala Gly Gly
 225 230 235 240

Ser Phe Gly Glu Leu Ala Leu Met Tyr Asn Ala Pro Arg Ala Ala Thr
 245 250 255

Ile Ile Thr Thr Ser Asp Ser Val Leu Trp Ala Leu Asp Arg Asn Thr
 260 265 270

Ser Ala Pro Ser Leu Met Glu Asn Thr Ser Arg Lys Arg Arg Met Tyr
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Glu Tyr Phe Leu Ser Glu Val Val Leu Leu Lys Ser Leu Glu Ser Tyr
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Glu Gln His Lys Ile Ala Asp Ala Leu Glu Ser Val Tyr Phe Glu Asp
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Gly Gln Glu Val Val Lys Gln Gly Asp Val Gly Asp Gln Phe Tyr Ile
 325 330 335

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 340 345 350

Gln Gln Val Asn Gln Leu Glu Arg Gly Ser Tyr Phe Gly Glu Leu Ala
 355 360 365

Leu Leu Asn Asp Ala Pro Arg Ala Ala Thr Val Val Ala His Gly Arg
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Leu Lys Cys Ala Thr Leu Gly Lys Lys Ala Phe Thr Arg Leu Leu Gly
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 Ser Pro Ser Ser Gln Thr Xaa Met Asp Asp Phe Glu Ile Lys Gln Pro
 20 25 30

ata ggt aac aga tgg acg gca tct gca tgt act gtt act gat aga cac 144
 Ile Gly Asn Arg Trp Thr Ala Ser Ala Cys Thr Val Thr Asp Arg His
 35 40 45

ctg ctt caa ggc tac gga tca tct gcc atg gtt tat agc gca gtg tat 192
 Leu Leu Gln Gly Tyr Gly Ser Ser Ala Met Val Tyr Ser Ala Val Tyr
 50 55 60

ata cct cac aac aaa cgg gtc gcc atc aag gtg att gat ctg gac atg 240
 Ile Pro His Asn Lys Arg Val Ala Ile Lys Val Ile Asp Leu Asp Met
 65 70 75 80

ttt gag cgc aac caa ata gac gag ctg agg gta gtacatggca gcacacacta 293
 Phe Glu Arg Asn Gln Ile Asp Glu Leu Arg Val
 85 90

ggattccctt cttattgaca aaacgtatat atng aga gag aca gcc ttg atg gct 348
 Arg Glu Thr Ala Leu Met Ala
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ctg tcc aag cat cca cat gtg ttg cga gtc tac ggc tca ttt gtc cac 396
 Leu Ser Lys His Pro His Val Leu Arg Val Tyr Gly Ser Phe Val His
 100 105 110

gga tcc aag ctg tac att gtc act cct tat atg gca gta gga tcc tgt 444
 Gly Ser Lys Leu Tyr Ile Val Thr Pro Tyr Met Ala Val Gly Ser Cys
 115 120 125 130

ctc gat atc atg aag ttg agt ttc ccc gac ggc cta gac gag att agc 492
 Leu Asp Ile Met Lys Leu Ser Phe Pro Asp Gly Leu Asp Glu Ile Ser
 135 140 145

att gct act atc cta aaa cag gca ctg gaa gga cta gcc tat ttg cac 540
 Ile Ala Thr Ile Leu Lys Gln Ala Leu Glu Gly Leu Ala Tyr Leu His
 150 155 160

aaa aat ggc cac atc cat cga gac gta aag gca ggc aac ctg ctg atg 588
 Lys Asn Gly His Ile His Arg Asp Val Lys Ala Gly Asn Leu Leu Met
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 35 40 45

Leu Leu Gln Gly Tyr Gly Ser Ser Ala Met Val Tyr Ser Ala Val Tyr
 50 55 60

Ile Pro His Asn Lys Arg Val Ala Ile Lys Val Ile Asp Leu Asp Met
 65 70 75 80

Phe Glu Arg Asn Gln Ile Asp Glu Leu Arg Val Arg Glu Thr Ala Leu
 85 90 95

Met Ala Leu Ser Lys His Pro His Val Leu Arg Val Tyr Gly Ser Phe
 100 105 110

Val His Gly Ser Lys Leu Tyr Ile Val Thr Pro Tyr Met Ala Val Gly
 115 120 125

Ser Cys Leu Asp Ile Met Lys Leu Ser Phe Pro Asp Gly Leu Asp Glu
 130 135 140

Ile Ser Ile Ala Thr Ile Leu Lys Gln Ala Leu Glu Gly Leu Ala Tyr
 145 150 155 160

Leu His Lys Asn Gly His Ile His Arg Asp Val Lys Ala Gly Asn Leu
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Lys

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   1              5              10              15

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Glu Pro Lys Ile Cys Asp Phe Gly Leu Ala Arg Gly Tyr Ser Glu Asn
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tta aag cgc ttt gca tta cca ggc ggt tca gca gca gca gca ccc ggc 96
Leu Lys Arg Phe Ala Leu Pro Gly Gly Ser Ala Ala Ala Pro Gly
20 25 30
gga cga tgc ccc aac ggc agc ggc gag agc att tgc tgc gtc ttg tgg 144
Gly Arg Ser Pro Asn Gly Ser Gly Glu Ser Ile Ser Cys Val Leu Trp
35 40 45
aac gac ctg ttc ttc atc aca ggc acc gac att gtg cgc tgc ctg acc 192
Asn Asp Leu Phe Phe Ile Thr Gly Thr Asp Ile Val Arg Ser Leu Thr
50 55 60
ttt cgc ttc cat gcg ttt ggc cga ccc gtt acg aac gca aag aag ttt 240
Phe Arg Phe His Ala Phe Gly Arg Pro Val Thr Asn Ala Lys Lys Phe
65 70 75 80
gaa gag ggc ata ttt tct gat ttg cgc aac tta aaa cca ggt cat gat 288
Glu Glu Gly Ile Phe Ser Asp Leu Arg Asn Leu Lys Pro Gly His Asp
85 90 95
gct cgg ttg gag gaa ccc aaa tct gaa ttg ctg gac atg ctc tac aag 336
Ala Arg Leu Glu Glu Pro Lys Ser Glu Leu Leu Asp Met Leu Tyr Lys
100 105 110
aac aat tgc atc cgc aca caa aaa aaa caa aaa gta ttt ttc tgg ttt 384
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 35 40 45

Asn Asp Leu Phe Phe Ile Thr Gly Thr Asp Ile Val Arg Ser Leu Thr
 50 55 60

Phe Arg Phe His Ala Phe Gly Arg Pro Val Thr Asn Ala Lys Lys Phe
 65 70 75 80

Glu Glu Gly Ile Phe Ser Asp Leu Arg Asn Leu Lys Pro Gly His Asp
 85 90 95

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Ala Asp Phe Thr Asp Ser Leu Ile Lys Asn Ile Gly Val His Ser Ser	
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Ser Pro Val Met Thr Ser Val Asn Met Gly Gln Leu Gly Glu Lys Leu	
20 25 30	
cgt caa gct cgt aca aca aca ctt gct tcc tta tct caa gct ctt tca	680
Arg Gln Ala Arg Thr Thr Thr Leu Ala Ser Leu Ser Gln Ala Leu Ser	
35 40 45	
aag aag ccc gaa gct gct gct gct gct gcc act gcc ccc aac gct gtt	728
Lys Lys Pro Glu Ala Ala Ala Ala Ala Ala Thr Ala Pro Asn Ala Val	
50 55 60 65	
aat gaa agt acc acc aca ccc acc aca atg caa ctc cct gct tcg gaa	776
Asn Glu Ser Thr Thr Thr Pro Thr Thr Met Gln Leu Pro Ala Ser Glu	
70 75 80	
aaa gcc act agt caa ttg gag atc aat gtg gtt gaa gct cgt aat ttg	824
Lys Ala Thr Ser Gln Leu Glu Ile Asn Val Val Glu Ala Arg Asn Leu	
85 90 95	

acc att gct gat gcg cgc aaa gcc gac acc tac tgt att gtt cat tac	872
Thr Ile Ala Asp Ala Arg Lys Ala Asp Thr Tyr Cys Ile Val His Tyr	
100 105 110	
gaa ggc aac acc aca tca acg ctt gat aaa gta gat gat ggc atc ttg	920
Glu Gly Asn Thr Thr Ser Thr Leu Asp Lys Val Asp Asp Gly Ile Leu	
115 120 125	
ccc agc acg cct ctg gtg att aaa tct caa gtc gct agc ggt gca ttc	968
Pro Ser Thr Pro Leu Val Ile Lys Ser Gln Val Ala Ser Gly Ala Phe	
130 135 140 145	
aag gca ttt gaa atc atg atg agc gct agt tct ccc aag tgg atg cat	1016
Lys Ala Phe Glu Ile Met Met Ser Ala Ser Ser Pro Lys Trp Met His	
150 155 160	
cggt gtc aac ttg taagttgcta tccagaatat gtcaaaaagg gctctgcgct	1068
Arg Val Asn Leu	
165	
aaccatgtta ctatagt gat gta act gct ggt aac aag gag atc act gtg	1118
Asp Val Thr Ala Gly Asn Lys Glu Ile Thr Val	
170 175	
ttt gtc tat gat cgt ggt aac aaa ttg ccc aat ggt gaa gat cgc ttc	1166
Phe Val Tyr Asp Arg Gly Asn Lys Leu Pro Asn Gly Glu Asp Arg Phe	
180 185 190	
ttg ggc atg tct agc att gtt ccc aac ttg gtc aac aag aag acg gtc	1214
Leu Gly Met Ser Ser Ile Val Pro Asn Leu Val Asn Lys Lys Thr Val	
195 200 205	
gag ctg atc ttt cct ctt cac ggc cgt cct gac gat gat caa gaa gtt	1262
Glu Leu Ile Phe Pro Leu His Gly Arg Pro Asp Asp Asp Gln Glu Val	
210 215 220	
act ggt gat gtc cgt ctt caa gtt act ttt atc gac cct aaa aag	1307
Thr Gly Asp Val Arg Leu Gln Val Thr Phe Ile Asp Pro Lys Lys	
225 230 235	
gtaattttat atgagtatga ttcttgacag ctgatgtctg acacttctaa aaccctattc	1367
aag gct aat ctt aag cca gag gat ttc cgc att gtg cgt atg att ggt	1415
Ala Asn Leu Lys Pro Glu Asp Phe Arg Ile Val Arg Met Ile Gly	
240 245 250	
caa ggc tca gtg ggt aag gtg tat gag gtg atc aag cgt gat tct ggc	1463
Gln Gly Ser Val Gly Lys Val Tyr Glu Val Ile Lys Arg Asp Ser Gly	
255 260 265 270	
cgt acc tat gcc atg aag gtg ctc tct aag cgt ctc ttg ctc gcc gag	1511
Arg Thr Tyr Ala Met Lys Val Leu Ser Lys Arg Leu Leu Leu Ala Glu	
275 280 285	
aat gaa gtc gat act gcc ttc aac gag cgc aat gtg ctg gtt cag tct	1559
Asn Glu Val Asp Thr Ala Phe Asn Glu Arg Asn Val Leu Val Gln Ser	
290 295 300	

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aac cat ctc ttc ttg gtt atg gat tac ttt ccg ggt ggc gaa ttg ttt Asn His Leu Phe Leu Val Met Asp Tyr Phe Pro Gly Gly Glu Leu Phe 320 325 330	1655
gat ttc ctg gag cgt gag cgt tgt ttg agc gag aag cgt tgc caa ttc Asp Phe Leu Glu Arg Glu Arg Cys Leu Ser Glu Lys Arg Cys Gln Phe 335 340 345 350	1703
ttt gct gcc gag att gtg tgt gcc ttt gac aac atc cat gct cgc aac Phe Ala Ala Glu Ile Val Cys Ala Phe Asp Asn Ile His Ala Arg Asn 355 360 365	1751
att gtc tat cgt aac ctg aag cca gag agc atc ttg ctg gat gca cat Ile Val Tyr Arg Asn Leu Lys Pro Glu Ser Ile Leu Leu Asp Ala His 370 375 380	1799
gga cac att gcc ttg aca gat ttc ggc tta tgc aag caa ttg aag aac Gly His Ile Ala Leu Thr Asp Phe Gly Leu Cys Lys Gln Leu Lys Asn 385 390 395	1847
aag atg gat ttg att caa ggt gtg cct caa gtc att aca caa gaa tac Lys Met Asp Leu Ile Gln Gly Val Pro Gln Val Ile Thr Gln Glu Tyr 400 405 410	1895
ctc gcc cct gaa atg gta atg caa aag ccc tat ggc atg gct gcc gac Leu Ala Pro Glu Met Val Met Gln Lys Pro Tyr Gly Met Ala Ala Asp 415 420 425 430	1943
tgg tgg agt ctc ggt gtt ttg atg ttt gag ctg ttg act gga tct cct Trp Trp Ser Leu Gly Val Leu Met Phe Glu Leu Leu Thr Gly Ser Pro 435 440 445	1991
cct ttc cat tct gtt gaa caa ggt gaa ttg ttt aga caa atc ctg gaa Pro Phe His Ser Val Glu Gln Gly Glu Leu Phe Arg Gln Ile Leu Glu 450 455 460	2039
gct ccc att aaa ttc cct gct ggg ggc tgc att aca gag gaa gcc aag Ala Pro Ile Lys Phe Pro Ala Gly Gly Cys Ile Thr Glu Glu Ala Lys 465 470 475	2087
gat ttc atc tgc caa ctg ctg gag cgt gat cct gcc aag cgt ctg ggc Asp Phe Ile Cys Gln Leu Leu Glu Arg Asp Pro Ala Lys Arg Leu Gly 480 485 490	2135
tcc cat ggt gat gtt gct cag gtc aaa gca cat cca ttc ttt aag gat Ser His Gly Asp Val Ala Gln Val Lys Ala His Pro Phe Phe Lys Asp 495 500 505 510	2183
ctc aac tgg gat gtc gtt tac aag aag caa atg cag ctt ccc ttt gtg Leu Asn Trp Asp Val Val Tyr Lys Lys Gln Met Gln Leu Pro Phe Val 515 520 525	2231
ccc gag gta gaa gag cag ctc cgc gaa gaa gcc att gct gct gct gct	2279

Pro Glu Val Glu Glu Gln Leu Arg Glu Glu Ala Ile Ala Ala Ala Ala
 530 535 540

gcc att agc att cct gtg acc aac agc aag acc gag tct acc aat gcc 2327
 Ala Ile Ser Ile Pro Val Thr Asn Ser Lys Thr Glu Ser Thr Asn Ala
 545 550 555

aat gtg atg cct gtg gct gat caa tcc aaa ttc aag gga ttt agc tat 2375
 Asn Val Met Pro Val Ala Asp Gln Ser Lys Phe Lys Gly Phe Ser Tyr
 560 565 570

att cgt gaa gat gtc atg gca aag aag ggc gag cat cgt ctg ggt gtc 2423
 Ile Arg Glu Asp Val Met Ala Lys Lys Gly Glu His Arg Leu Gly Val
 575 580 585 590

aat cct gag gat gaa gat ccc gaa gtt gat ttc tgg ttt aga cag 2468
 Asn Pro Glu Asp Glu Asp Pro Glu Val Asp Phe Trp Phe Arg Gln
 595 600 605

taaaaatcgt ccatctatcc ttacattttg tacatatata ttaatcaaga cccccctcct 2528
 cattcaataa agcacatatt tgttcatata ccaaaaaaaaa aaaaaaaaaa 2578

<210> 12
 <211> 605
 <212> PRT
 <213> Mucor circinelloides

<400> 12

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Ser Ser Pro Val Met Thr Ser Val Asn Met Gly Gln Leu Gly Glu Lys
 20 25 30

Leu Arg Gln Ala Arg Thr Thr Thr Leu Ala Ser Leu Ser Gln Ala Leu
 35 40 45

Ser Lys Lys Pro Glu Ala Ala Ala Ala Ala Ala Thr Ala Pro Asn Ala
 50 55 60

Val Asn Glu Ser Thr Thr Thr Pro Thr Thr Met Gln Leu Pro Ala Ser
 65 70 75 80

Glu Lys Ala Thr Ser Gln Leu Glu Ile Asn Val Val Glu Ala Arg Asn
 85 90 95

Leu Thr Ile Ala Asp Ala Arg Lys Ala Asp Thr Tyr Cys Ile Val His
 100 105 110

Tyr Glu Gly Asn Thr Thr Ser Thr Leu Asp Lys Val Asp Asp Gly Ile
 115 120 125

Leu Pro Ser Thr Pro Leu Val Ile Lys Ser Gln Val Ala Ser Gly Ala
 130 135 140

Phe Lys Ala Phe Glu Ile Met Met Ser Ala Ser Ser Pro Lys Trp Met
 145 150 155 160

His Arg Val Asn Leu Asp Val Thr Ala Gly Asn Lys Glu Ile Thr Val
 165 170 175

Phe Val Tyr Asp Arg Gly Asn Lys Leu Pro Asn Gly Glu Asp Arg Phe
 180 185 190

Leu Gly Met Ser Ser Ile Val Pro Asn Leu Val Asn Lys Lys Thr Val
 195 200 205

Glu Leu Ile Phe Pro Leu His Gly Arg Pro Asp Asp Asp Gln Glu Val
 210 215 220

Thr Gly Asp Val Arg Leu Gln Val Thr Phe Ile Asp Pro Lys Lys Ala
 225 230 235 240

Asn Leu Lys Pro Glu Asp Phe Arg Ile Val Arg Met Ile Gly Gln Gly
 245 250 255

Ser Val Gly Lys Val Tyr Glu Val Ile Lys Arg Asp Ser Gly Arg Thr
 260 265 270

Tyr Ala Met Lys Val Leu Ser Lys Arg Leu Leu Leu Ala Glu Asn Glu
 275 280 285

Val Asp Thr Ala Phe Asn Glu Arg Asn Val Leu Val Gln Ser Leu Ser
 290 295 300

Ser Pro Phe Ile Ala Asn Leu Lys Tyr Ser Phe Gln Thr Thr Asn His
 305 310 315 320

Leu Phe Leu Val Met Asp Tyr Phe Pro Gly Gly Glu Leu Phe Asp Phe
 325 330 335

Leu Glu Arg Glu Arg Cys Leu Ser Glu Lys Arg Cys Gln Phe Phe Ala

340					345					350					
Ala	Glu	Ile	Val	Cys	Ala	Phe	Asp	Asn	Ile	His	Ala	Arg	Asn	Ile	Val
	355						360					365			
Tyr	Arg	Asn	Leu	Lys	Pro	Glu	Ser	Ile	Leu	Leu	Asp	Ala	His	Gly	His
	370					375					380				
Ile	Ala	Leu	Thr	Asp	Phe	Gly	Leu	Cys	Lys	Gln	Leu	Lys	Asn	Lys	Met
385						390					395				400
Asp	Leu	Ile	Gln	Gly	Val	Pro	Gln	Val	Ile	Thr	Gln	Glu	Tyr	Leu	Ala
			405						410					415	
Pro	Glu	Met	Val	Met	Gln	Lys	Pro	Tyr	Gly	Met	Ala	Ala	Asp	Trp	Trp
			420					425					430		
Ser	Leu	Gly	Val	Leu	Met	Phe	Glu	Leu	Leu	Thr	Gly	Ser	Pro	Pro	Phe
	435						440					445			
His	Ser	Val	Glu	Gln	Gly	Glu	Leu	Phe	Arg	Gln	Ile	Leu	Glu	Ala	Pro
	450					455					460				
Ile	Lys	Phe	Pro	Ala	Gly	Gly	Cys	Ile	Thr	Glu	Glu	Ala	Lys	Asp	Phe
465						470					475				480
Ile	Cys	Gln	Leu	Leu	Glu	Arg	Asp	Pro	Ala	Lys	Arg	Leu	Gly	Ser	His
			485						490					495	
Gly	Asp	Val	Ala	Gln	Val	Lys	Ala	His	Pro	Phe	Phe	Lys	Asp	Leu	Asn
			500					505					510		
Trp	Asp	Val	Val	Tyr	Lys	Lys	Gln	Met	Gln	Leu	Pro	Phe	Val	Pro	Glu
	515						520					525			
Val	Glu	Glu	Gln	Leu	Arg	Glu	Glu	Ala	Ile	Ala	Ala	Ala	Ala	Ala	Ile
	530					535					540				
Ser	Ile	Pro	Val	Thr	Asn	Ser	Lys	Thr	Glu	Ser	Thr	Asn	Ala	Asn	Val
545						550					555				560
Met	Pro	Val	Ala	Asp	Gln	Ser	Lys	Phe	Lys	Gly	Phe	Ser	Tyr	Ile	Arg
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Glu Asp Val Met Ala Lys Lys Gly Glu His Arg Leu Gly Val Asn Pro
 580 585 590

Glu Asp Glu Asp Pro Glu Val Asp Phe Trp Phe Arg Gln
 595 600 605

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 <212> DNA
 <213> *Mucor circinelloides*

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 caacaagagc cattaacgtg gacagatttg cccttttgta agtactcaaa ttagtcaagt 180
 gatagactca cacactcaca ctacacacaa cctctagatg aagatccctc tctcatgatg 240
 acaccaacta caccatctat atttacagct aataacaaca acccctatga tatcccttct 300
 tctgcctcaa atgctacaca caccgcatct actacacata ctactaatac acaaatcata 360
 tctgccgaag cactgcaaatt tggtagctgg aagagaatga catttgaacc caatgacctc 420
 tcatgccagt tcgatagaga cagcaaactc ttcagctggg gcatccaaga cggtatttcc 480
 aagttcaaaa tggaattccc acaagaatth gtgcaatcca tcaagctatc acccttaaca 540
 agtcgacctg gctgggcaga ttggagatga atgtactatc tactcaacac atcttggtct 600
 acatggagac gccgcaacaa agctggattc aatgccgcga ctacactgaa gacaagcagg 660
 cttccatcat cagcctgcac caactagacg gccctgcact tgcattaaag gcagaactag 720
 aatccctctc taaggaaaac gactatctag ctaccatcat tcattaatth gcatatcatt 780
 gattgggtgcg cctgattaaa attgtgtaat ataaaatacc atgttgacct ctccccctcc 840
 atttttctct tcttcttctt cttcaacctt tgttgcttat tctcccttaa cttttgaata 900
 aatcaactth ctaaacaccc tataaaa 927

<210> 14
 <211> 419
 <212> DNA
 <213> *Mucor circinelloides*

<400> 14
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 tcactcattc caaagaaagt attccttgga tctcaaatgc aatccaatgg aaaacagatg 120

cttgggtcgt cttggtggca taaattggaa aaactggggt ttccgttcat aaggtcccat 180
 ttccgtgga aagtctaaaa tcgactgact tttttccaat gaggaaagcc tggaggaggt 240
 cgacttgat cacaacaagg ttgcttatga aatcaacaga gtcacatccc gtctaaaacc 300
 cagtttggat ccgttttctt cgcttctatc tgtgggtgog aggatttggg ataaaaagga 360
 ctagattctc cacaacaatt tccatttttt ccctcattat cattcaataa tactgtaaa 419

<210> 15
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> n is a, c, g or t

<220>
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 <222> (18)..(18)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (21)..(21)
 <223> n is a, c, g or t

<400> 15
 ggngaytayt tytaygtngt ngar 24

<210> 16
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer

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 <223> n is a, c, g or t

<220>
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 <222> (7)..(7)
 <223> n is a, c, g or t

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 <223> n is a, c, g or t

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 <223> n is a, c, g or t

<220>
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 <222> (19)..(19)
 <223> n is a, c, g or t

<400> 16
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24

<210> 17
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<400> 17
 actgcctcga gatgatcact gacgaacatc cgtttg

36

<210> 18
 <211> 42
 <212> DNA
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<220>
 <223> oligonucleotide primer

<400> 18
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42

<210> 19
 <211> 21
 <212> DNA
 <213> Artificial Sequence

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 <223> oligonucleotide primer

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 <223> n is a, c, g or t

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 <223> n is a, c, g or t

<220>
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 <223> n is a, c, g or t

<400> 19
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21

<210> 20
 <211> 24
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 <223> n is a, c, g or t

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 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (19)..(19)
 <223> n is a, c, g or t

<400> 20
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24

<210> 21
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<220>
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 <222> (13)..(13)

<223> n is a, c, g or t

<220>

<221> misc_feature

<222> (31)..(31)

<223> n is a, c, g or t

<400> 21

raaccaraar aanacyttyt gytttyttytg ng

33

<210> 22

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer

<220>

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<222> (9)..(9)

<223> n is a, c, g or t

<400> 22

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21

<210> 23

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer

<220>

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<222> (10)..(10)

<223> n is a, c, g or t

<220>

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<222> (13)..(13)

<223> n is a, c, g or t

<220>

<221> misc_feature

<222> (16)..(16)

<223> n is a, c, g or t

<400> 23

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24

<210> 24

<211> 2471
 <212> DNA
 <213> *Mucor circinelloides*

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 <222> (742)..(1038)

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 <222> (1096)..(1668)

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 <222> (1669)..(1724)

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 tattatctgt ttcattgtaa aaaaaactct gttgtggtac aaacattagt gtgaaccacg 180
 cgcagccata ccactagtca aaataatgct ctactgcaaa aaatgacggt tgacgaataa 240
 tgcaacgtaa agatgggttta gaaacccttg atatccaaat tacacgtgta gcagccttcg 300
 tgggtatatt tcatcacaac actactaggt agctcaggga tagttcaaac gggcaatttc 360
 catcctcatc acactttatt caccaaggaa agaagtgaat tggcatcttc tatcgttcaa 420
 catctacagg gacatctgtg agatacatct gattgctcga caagcggaca atagatgaca 480
 cgttatcaat gctatcactc taaaatgtca tgtctgactg agtccattgc aatcatcact 540
 ccatccgaca tcaggtcaca atttatgctt ctattttcca atggatccga atccgattca 600
 aacaagatta attctccctc aaaataccca tgaagtgtga gacattgcga aatgttatat 660

aaacccaatg catttctcgt ctttcagggg ttttttcttc ttcttcatac tatatctcta	720
tatatatttat aaattctaac a atg gtt gtt caa gtc ggt att aac ggt ttc	771
Met Val Val Gln Val Gly Ile Asn Gly Phe	
1 5 10	
ggg cgt att ggt cgt att gtc ctt cgt gct act gag tcc aac aag gat	819
Gly Arg Ile Gly Arg Ile Val Leu Arg Ala Thr Glu Ser Asn Lys Asp	
15 20 25	
gtc caa gtt gtt gct atc aac gat ccc ttc att cct ctc gac tat atg	867
Val Gln Val Val Ala Ile Asn Asp Pro Phe Ile Pro Leu Asp Tyr Met	
30 35 40	
gtc tac atg ttg aag tac gat act gtt cac ggt cgt ttc gat ggt tcc	915
Val Tyr Met Leu Lys Tyr Asp Thr Val His Gly Arg Phe Asp Gly Ser	
45 50 55	
gtc gag gcc aag gat ggt aag ctc gtt gtc aac ggt cat gct atc gcc	963
Val Glu Ala Lys Asp Gly Lys Leu Val Val Asn Gly His Ala Ile Ala	
60 65 70	
gtc tct gct gag cgc gat cct acc tct att cct tgg ggt tcc gct ggt	1011
Val Ser Ala Glu Arg Asp Pro Thr Ser Ile Pro Trp Gly Ser Ala Gly	
75 80 85 90	
gct gac tac gtt gtc gag tcc act ggg taaatatact gaaatgcatt	1058
Ala Asp Tyr Val Val Glu Ser Thr Gly	
95	
atatctcgaa tatctaattct aacattgacg taatagt gtc ttc act acc act gaa	1113
Val Phe Thr Thr Thr Glu	
100 105	
gct gcc tct gct cat ctt aag ggt ggt gcc aag aag gtc atc atc tct	1161
Ala Ala Ser Ala His Leu Lys Gly Gly Ala Lys Lys Val Ile Ile Ser	
110 115 120	
gct ccc tct gct gat gcc ccc atg ttc gtc tgt ggt gtc aac ctc gaa	1209
Ala Pro Ser Ala Asp Ala Pro Met Phe Val Cys Gly Val Asn Leu Glu	
125 130 135	
gct tac aag tct gaa tac aag gtt atc tcc aac gcc tct tgt acc acc	1257
Ala Tyr Lys Ser Glu Tyr Lys Val Ile Ser Asn Ala Ser Cys Thr Thr	
140 145 150	
aac tgt ttg gct ccc ctc gcc aag gtc att aac gat aac ttt ggt atc	1305
Asn Cys Leu Ala Pro Leu Ala Lys Val Ile Asn Asp Asn Phe Gly Ile	
155 160 165	
gct gat ggt ttg atg acc act gtc cac gcc acc act gcc acc caa aag	1353
Ala Asp Gly Leu Met Thr Thr Val His Ala Thr Thr Ala Thr Gln Lys	
170 175 180 185	
act gtc gat ggt ccc tct cac aag gat tgg aga ggt ggt cgt gcc gct	1401
Thr Val Asp Gly Pro Ser His Lys Asp Trp Arg Gly Gly Arg Ala Ala	
190 195 200	

gct gcc aac atc atc ccc tct tcc act ggt gct gcc aag gct gtc ggt Ala Ala Asn Ile Ile Pro Ser Ser Thr Gly Ala Ala Lys Ala Val Gly 205 210 215	1449
aag gtc att ccc gct ctc aac ggt aag ctc act ggt atg gct ttc cgt Lys Val Ile Pro Ala Leu Asn Gly Lys Leu Thr Gly Met Ala Phe Arg 220 225 230	1497
gtc ccc acc ccc gat gtc tct gtc gtt gat ttg acc gtc aac ctc tcc Val Pro Thr Pro Asp Val Ser Val Val Asp Leu Thr Val Asn Leu Ser 235 240 245	1545
aag ggt gct tct tat gat gaa atc aag caa gcc atc aag aag gcc tct Lys Gly Ala Ser Tyr Asp Glu Ile Lys Gln Ala Ile Lys Lys Ala Ser 250 255 260 265	1593
gaa act acc atg aag ggt gtc ctc ggt tac act tct gat gct gtt gtc Glu Thr Thr Met Lys Gly Val Leu Gly Tyr Thr Ser Asp Ala Val Val 270 275 280	1641
agc agt gat ttc gtg ggt gaa gtt tgg taagaaacgt tattatttca Ser Ser Asp Phe Val Gly Glu Val Trp 285 290	1688
tcgtttgaat agtttactaa cattgaaaat catagt tct tcc gta ttt gac gct Ser Ser Val Phe Asp Ala 295	1742
gct gcc ggt atc caa ttg acc ccc act ttt gtt aag ctt atc gct tgg Ala Ala Gly Ile Gln Leu Thr Pro Thr Phe Val Lys Leu Ile Ala Trp 300 305 310	1790
tat gac aat gag tat ggt tac tct aac cgt gtc gtt gac ctc ctc gtt Tyr Asp Asn Glu Tyr Gly Tyr Ser Asn Arg Val Val Asp Leu Leu Val 315 320 325	1838
cat gcc gct aag gtc gat ggt gct ctc taaatcgtaa atcatttcta His Ala Ala Lys Val Asp Gly Ala Leu 330 335	1885
gtcattgcat ttcatacaca catctgttac ataaataaac ttcattgtaaa aagtcggtca	1945
taagatcggt ttttgtaaat tagcttatat taatttctgt tccaaccctc tgatatgtaa	2005
aatgttgacg aattgcaagt attttgacag gcagaatgac agcatatatt tgangcctgt	2065
gvacaatctg tggtacataa gattcctggt aaaggatgga tgatattata ttttacagtt	2125
ataagagccg gtattggcac acgaaggaag ccttgcagcg agaaggacga cgctcttttt	2185
tataggctca tcaactcaatg agagttgcag gaagcactat tttgtaaatg cctgaaatac	2245
agagaccctc tggactatta ttctcaagaa gcactttaac aagaaaaata tagttctttt	2305
gctaatttca agaccttaat catatatnnc gctttcattt ttatttcatg gtttcattca	2365
atttatagat gtattactac actactgatt gctgttactg ttactatcgc cctggccatt	2425

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2471

<210> 25
 <211> 337
 <212> PRT
 <213> Mucor circinelloides

<400> 25

Met Val Val Gln Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Ile
 1 5 10 15

Val Leu Arg Ala Thr Glu Ser Asn Lys Asp Val Gln Val Val Ala Ile
 20 25 30

Asn Asp Pro Phe Ile Pro Leu Asp Tyr Met Val Tyr Met Leu Lys Tyr
 35 40 45

Asp Thr Val His Gly Arg Phe Asp Gly Ser Val Glu Ala Lys Asp Gly
 50 55 60

Lys Leu Val Val Asn Gly His Ala Ile Ala Val Ser Ala Glu Arg Asp
 65 70 75 80

Pro Thr Ser Ile Pro Trp Gly Ser Ala Gly Ala Asp Tyr Val Val Glu
 85 90 95

Ser Thr Gly Val Phe Thr Thr Thr Glu Ala Ala Ser Ala His Leu Lys
 100 105 110

Gly Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro
 115 120 125

Met Phe Val Cys Gly Val Asn Leu Glu Ala Tyr Lys Ser Glu Tyr Lys
 130 135 140

Val Ile Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala
 145 150 155 160

Lys Val Ile Asn Asp Asn Phe Gly Ile Ala Asp Gly Leu Met Thr Thr
 165 170 175

Val His Ala Thr Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser His
 180 185 190

Lys Asp Trp Arg Gly Gly Arg Ala Ala Ala Ala Asn Ile Ile Pro Ser
 195 200 205

Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Ala Leu Asn
 210 215 220

Gly Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Pro Asp Val Ser
 225 230 235 240

Val Val Asp Leu Thr Val Asn Leu Ser Lys Gly Ala Ser Tyr Asp Glu
 245 250 255

Ile Lys Gln Ala Ile Lys Lys Ala Ser Glu Thr Thr Met Lys Gly Val
 260 265 270

Leu Gly Tyr Thr Ser Asp Ala Val Val Ser Ser Asp Phe Val Gly Glu
 275 280 285

Val Trp Ser Ser Val Phe Asp Ala Ala Ala Gly Ile Gln Leu Thr Pro
 290 295 300

Thr Phe Val Lys Leu Ile Ala Trp Tyr Asp Asn Glu Tyr Gly Tyr Ser
 305 310 315 320

Asn Arg Val Val Asp Leu Leu Val His Ala Ala Lys Val Asp Gly Ala
 325 330 335

Leu

<210> 26
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (15)..(15)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (18)..(18)
 <223> n is a, c, g or t

<220>
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 <222> (21)..(21)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (24)..(24)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (27)..(27)
 <223> n is a, c, g or t

<400> 26
 aarttyttyy tngcnacngc nccngtnaay tgg

33

<210> 27
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (6)..(6)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (9)..(9)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (18)..(18)
 <223> n is a, c, g or t

<400> 27
ccnggnmgng tnaayytnat hgg

23

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (9)..(9)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (15)..(15)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (18)..(18)
<223> n is a, c, g or t

<400> 28
ccnccccanc cngcncngt

20

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<220>
<221> misc_feature
<222> (9)..(9)
<223> n is a, c, g or t

<220>

<221> misc_feature
 <222> (18)..(18)
 <223> n is a, c, g or t

<400> 29
 garcayggna thcarccnga ygg

23

<210> 30
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<220>
 <221> misc_feature
 <222> (4)..(4)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (13)..(13)
 <223> n is a, c, g or t

<400> 30
 catnccytcn ccnacrtaac a

21

<210> 31
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<400> 31
 catccttggtt ggactcagta gc

22

<210> 32
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<400> 32
 cttcaggggtt agagagagaa gc

22

<210> 33
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<400> 33
 ccttgggggtt ttcgagggag g 21

<210> 34
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<400> 34
 actgcggagc tcattatgat cactgacgaa catccg 36

<210> 35
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<400> 35
 gcgcatgctt atgattgctg gttaatgac 29

<210> 36
 <211> 427
 <212> PRT
 <213> Mucor circinelloides

<400> 36

Met Ile Thr Asp Glu His Pro Phe Glu Phe Ala Pro Gln Gln Asp Glu
 1 5 10 15

Tyr Thr Gln Leu Leu Thr Glu Leu His Asn Glu Tyr Cys Ala Glu Gln
 20 25 30

Pro Leu Asp Val Leu Gln Phe Cys Ser Asn Phe Phe Ile Arg Lys Leu
 35 40 45

Glu Glu Gln Arg Leu Glu His Arg Asn Asn His His Ser Arg Asn Asn

50	55	60
Leu Phe Asp Thr Asn Asp Thr Ser Asn Asp	Leu His Pro Leu Cys Glu	
65	70	75 80
Gln Pro Gln Glu Asp Phe Ser Gln Gln Gln Gly Ile Gln Trp Glu Thr		
	85	90 95
Thr His Met Gly His Pro Asn Asp His Gly Ala Leu His Asp Asp Asp		
	100	105 110
Asp Asp Pro Leu Glu Asp Glu Asp Asp Glu Glu Phe Asp Lys Phe Ser		
	115	120 125
Thr Glu Pro Leu Pro Ser Leu Pro Pro Thr Asn Tyr Asn Arg Gly Arg		
	130	135 140
Arg Thr Ser Val Lys Cys Arg Glu His Gly Thr Gln Arg Gln Pro Arg		
	145	150 155 160
Leu Cys Gln Gly His His Pro Gln Ile Ser Gly Thr Ser Glu Arg Ile		
	165	170 175
Lys Val Ser Ile Ser Asn Asn Phe Leu Phe Arg Asn Leu Asp Glu Glu		
	180	185 190
Gln Tyr Leu Asp Val Val Asn Ala Met Ser Glu Lys Arg Val Val Lys		
	195	200 205
Gly Thr Thr Val Ile Glu Gln Gly Ser Val Gly Asp Phe Phe Tyr Val		
	210	215 220
Val Glu Ser Gly Thr Leu Asp Cys Phe Ile Gly Gln Asn Lys Val Thr		
	225	230 235 240
Asn Tyr Glu Ala Gly Gly Ser Phe Gly Glu Leu Ala Leu Met Tyr Asn		
	245	250 255
Ala Pro Arg Ala Ala Thr Ile Ile Thr Thr Ser Asp Ser Val Leu Trp		
	260	265 270
Ala Leu Asp Arg Asn Thr Ser Ala Pro Ser Leu Met Glu Asn Thr Ser		
	275	280 285

Arg Lys Arg Arg Met Tyr Glu Tyr Phe Leu Ser Glu Val Val Leu Leu
290 295 300

Lys Ser Leu Glu Ser Tyr Glu Gln His Lys Ile Ala Asp Ala Leu Glu
305 310 315 320

Ser Val Tyr Phe Glu Asp Gly Gln Glu Val Val Lys Gln Gly Asp Val
325 330 335

Gly Asp Gln Phe Tyr Ile Ile Glu Ser Gly Glu Ala Ile Val Leu Lys
340 345 350

Glu Glu Asn Gly Val Gln Gln Gln Val Asn Gln Leu Glu Arg Gly Ser
355 360 365

Tyr Phe Gly Glu Leu Ala Leu Leu Asn Asp Ala Pro Arg Ala Ala Thr
370 375 380

Val Val Ala His Gly Arg Leu Lys Cys Ala Thr Leu Gly Lys Lys Ala
385 390 395 400

Phe Thr Arg Leu Leu Gly Pro Val Leu Asp Ile Leu Lys Arg Asn Ser
405 410 415

Glu Asn Tyr His Ala Val Ile Asn Gln Gln Ser
420 425

<210> 37
<211> 411
<212> PRT
<213> Aspergillus niger

<400> 37

Met Ala Glu Ser Ala Phe Pro Ser Ala Gln Gln Pro Leu Arg Val Gly
1 5 10 15

Thr Lys Asp Asp Lys Ala Ala Ala Phe Gln Lys Ile Ser Glu Glu Asp
20 25 30

Glu Tyr Glu Val Thr Ser Pro Thr Asp Pro Thr Phe Arg Ser Ala Asn
35 40 45

Ala Ala Ala Ala Ser Ser Ser Thr Gly Ser Pro Phe Phe Gly Gly Ser
50 55 60

Tyr Gly Glu Asn Ser Gly Pro Ile Arg Phe Asn Arg Ser Pro Phe Asp
 65 70 75 80

Asn Gly Pro Arg Glu Glu Asp Glu Glu Gly Ala Asp Glu Phe Pro Pro
 85 90 95

Glu Asp Ile Arg Pro Thr Gly Ala Ala Asn Gln Gly Phe Pro Asn Asn
 100 105 110

Tyr Ala Leu Gly Arg Arg Thr Ser Val Ser Ala Glu Ser Leu Asn Pro
 115 120 125

Thr Ser Ala Gly Ser Asp Ser Trp Thr Pro Pro Tyr His Glu Lys Thr
 130 135 140

Glu Glu Gln Leu Ser Arg Leu Lys Thr Ala Val Ser Ser Asn Phe Leu
 145 150 155 160

Phe Ser His Leu Asp Asp Asp Gln Phe Lys Ser Val Leu Asp Ala Leu
 165 170 175

Val Glu Lys Pro Ile Pro Ala Lys Gly Ile Lys Val Ile Ser Gln Gly
 180 185 190

Asp Ala Gly Asp Tyr Phe Tyr Ile Val Glu Asn Gly His Phe Asp Phe
 195 200 205

Met Ile His Pro Ser Gly Ser Val Gln Pro Gly Pro Asp Gly Met Gly
 210 215 220

Asn Lys Val Gly Ser Val Gly Pro Gly Gly Ser Phe Gly Glu Leu Ala
 225 230 235 240

Leu Met Tyr Asn Ala Pro Arg Ala Ala Thr Val Val Ser Val Asp Pro
 245 250 255

Lys Ser Thr Leu Trp Ala Leu Asp Arg Ile Thr Phe Arg Arg Ile Leu
 260 265 270

Met Asp Ser Ala Phe Gln Arg Arg Arg Met Tyr Glu Ala Phe Leu Glu
 275 280 285

Glu Val Pro Leu Leu Ser Ser Leu Lys Pro Tyr Glu Arg Ala Lys Ile
290 295 300

Ala Asp Ala Leu Asp Ala Ile Lys Tyr Pro Ala Gly Ser Thr Ile Ile
305 310 315 320

Ala Glu Gly Asp Pro Gly Asp Ala Phe Tyr Leu Leu Glu Ser Gly Glu
325 330 335

Ala Asp Ala Phe Lys Asn Gly Val Glu Gly Pro Val Lys Ser Tyr Lys
340 345 350

Arg Gly Asp Tyr Phe Gly Glu Leu Ala Leu Leu Asp Asp Lys Pro Arg
355 360 365

Ala Ala Ser Ile Val Ala Lys Thr Asp Val Lys Val Ala Lys Leu Gly
370 375 380

Arg Asp Gly Phe Lys Arg Leu Leu Gly Pro Val Glu Asp Ile Met Arg
385 390 395 400

Arg Ala Glu Tyr Glu Ser Asn Pro Val Pro Ala
405 410

<210> 38

<211> 403

<212> PRT

<213> Blastocadiella emersonii

<400> 38

Met Ala Asp Tyr Thr Ile Pro Ser Glu Leu Pro Pro Ile Leu Lys Asp
1 5 10 15

Leu Ser Arg Glu Val Leu Arg His Gln Pro Ala Asp Leu Val Gln Phe
20 25 30

Cys His Asp Tyr Phe Ala Lys Leu Leu Ala Gln Gln Arg Lys Val Leu
35 40 45

Met Asp Ser Ala Asp Pro Ala Thr Lys Ala Thr Ile Ala Ser Thr Ala
50 55 60

Gly Pro Ala Val Asp Ala Asp Glu Ala Ala Arg Ala Asn Ser Tyr Ala
65 70 75 80

Tyr Ser Thr Asp Asp Gly Phe Gly Thr Glu Asp Asp Asp Asp Asp Asp
 85 90 95

Asp Asp Glu Asp Asp Glu Ala Ala Ile Pro Pro Pro Val Val Asn Arg
 100 105 110

Gly Arg Arg Thr Ser Val Ser Ala Glu Ser Met Ala Pro Thr Ala His
 115 120 125

Asp Val Asp Ala Val Lys Thr Val Ile Pro Lys Ser Asp Glu Gln Arg
 130 135 140

Ala Arg Ile Gln Ala Ser Ile Gly Asn Asn Phe Leu Phe Arg Asn Leu
 145 150 155 160

Asp Glu Asp Gln Tyr Thr Asp Val Val Asn Ala Met Ala Glu Lys Lys
 165 170 175

Val Ala Ala Gly Glu Val Val Ile Arg Gln Gly Gly Val Gly Asp Tyr
 180 185 190

Phe Tyr Val Val Glu Thr Gly Ala Leu Asp Val Phe Val Asn Arg Asn
 195 200 205

Gly Asn Gly Asp Val Lys Val Thr Asp Tyr Ser Ala Gly Gly Ser Phe
 210 215 220

Gly Glu Leu Ala Leu Met Tyr Asn Ala Pro Arg Ala Ala Thr Val Val
 225 230 235 240

Ala Thr Ala Glu Ser Val Leu Trp Ala Leu Asp Arg Val Thr Phe Arg
 245 250 255

Arg Ile Leu Met Asp His Thr Ser Arg Lys Arg Arg Met Tyr Glu Ala
 260 265 270

Phe Leu Glu Glu Val Pro Leu Leu Ser Ser Leu Glu Pro Tyr Glu Arg
 275 280 285

His Lys Ile Ala Asp Ala Leu Glu Ser Val Ala Tyr Ala Asp Gly Asp
 290 295 300

Val Val Ile Arg Gln Gly Asp Val Gly Glu Asn Phe Tyr Ile Ile Glu

[illegible]

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<210> 39
<211> 459
<212> PRT
<213> Candida albicans
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<400> 39

Met	Ser	Asn	Pro	Gln	Gln	Gln	Phe	Ile	Ser	Asp	Glu	Leu	Ser	Gln	Leu	
1				5					10					15		
	Gln	Lys	Glu	Ile	Ile	Ser	Lys	Asn	Pro	Gln	Asp	Val	Leu	Gln	Phe	Cys
			20					25						30		
Ala	Asn	Tyr	Phe	Asn	Thr	Lys	Leu	Gln	Ala	Gln	Arg	Ser	Glu	Leu	Trp	
		35					40					45				
Ser	Gln	Gln	Ala	Lys	Ala	Glu	Ala	Ala	Gly	Ile	Asp	Leu	Phe	Pro	Ser	
	50					55					60					
Val	Asp	His	Val	Asn	Val	Asn	Ser	Ser	Gly	Val	Ser	Ile	Val	Asn	Asp	
65				70						75					80	
Arg	Gln	Pro	Ser	Phe	Lys	Ser	Pro	Phe	Gly	Val	Asn	Asp	Pro	His	Ser	
				85					90					95		

Asn His Asp Glu Asp Pro His Ala Lys Asp Thr Lys Thr Asp Thr Ala
 100 105 110

Ala Ala Ala Val Gly Gly Gly Ile Phe Lys Ser Asn Phe Asp Val Lys
 115 120 125

Lys Ser Ala Ser Asn Pro Pro Thr Lys Glu Val Asp Pro Asp Asp Pro
 130 135 140

Ser Lys Pro Ser Ser Ser Ser Gln Pro Asn Gln Gln Ser Ala Ser Ala
 145 150 155 160

Ser Ser Lys Thr Pro Ser Ser Lys Ile Pro Val Ala Phe Asn Ala Asn
 165 170 175

Arg Arg Thr Ser Val Ser Ala Glu Ala Leu Asn Pro Ala Lys Leu Lys
 180 185 190

Leu Asp Ser Trp Lys Pro Pro Val Asn Asn Leu Ser Ile Thr Glu Glu
 195 200 205

Glu Thr Leu Ala Asn Asn Leu Lys Asn Asn Phe Leu Phe Lys Gln Leu
 210 215 220

Asp Ala Asn Ser Lys Lys Thr Val Ile Ala Ala Leu Gln Gln Lys Ser
 225 230 235 240

Phe Ala Lys Asp Thr Val Ile Ile Gln Gln Gly Asp Glu Gly Asp Phe
 245 250 255

Phe Tyr Ile Ile Glu Thr Gly Thr Val Asp Phe Tyr Val Asn Asp Ala
 260 265 270

Lys Val Ser Ser Ser Ser Glu Gly Ser Ser Phe Gly Glu Leu Ala Leu
 275 280 285

Met Tyr Asn Ser Pro Arg Ala Ala Thr Ala Val Ala Ala Thr Asp Val
 290 295 300

Val Cys Trp Ala Leu Asp Arg Leu Thr Phe Arg Arg Ile Leu Leu Glu
 305 310 315 320

Gly Thr Phe Asn Lys Arg Leu Met Tyr Glu Asp Phe Leu Lys Asp Ile
 325 330 335

Glu Val Leu Lys Ser Leu Ser Asp His Ala Arg Ser Lys Leu Ala Asp
 340 345 350

Ala Leu Ser Thr Glu Met Tyr His Lys Gly Asp Lys Ile Val Thr Glu
 355 360 365

Gly Glu Gln Gly Glu Asn Phe Tyr Leu Ile Glu Ser Gly Asn Cys Gln
 370 375 380

Val Tyr Asn Glu Lys Leu Gly Asn Ile Lys Gln Leu Thr Lys Gly Asp
 385 390 395 400

Tyr Phe Gly Glu Leu Ala Leu Ile Lys Asp Leu Pro Arg Gln Ala Thr
 405 410 415

Val Glu Ala Leu Asp Asn Val Ile Val Ala Thr Leu Gly Lys Ser Gly
 420 425 430

Phe Gln Arg Leu Leu Gly Pro Val Val Glu Val Leu Lys Glu Gln Asp
 435 440 445

Pro Thr Lys Ser Gln Asp Pro Thr Ala Gly His
 450 455

<210> 40
 <211> 415
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 40

Val Ser Ser Leu Pro Lys Glu Ser Gln Ala Glu Leu Gln Leu Phe Gln
 1 5 10 15

Asn Glu Ile Asn Ala Ala Asn Pro Ser Asp Phe Leu Gln Phe Ser Ala
 20 25 30

Asn Tyr Phe Asn Lys Arg Leu Glu Gln Gln Arg Ala Phe Leu Lys Ala
 35 40 45

Arg Glu Pro Glu Phe Lys Ala Lys Asn Ile Val Leu Phe Pro Glu Pro
 50 55 60

Glu Glu Ser Phe Ser Arg Pro Gln Ser Ala Gln Ser Gln Ser Arg Ser

65		70		75		80
Arg Ser Ser Val Met Phe Lys Ser Pro Phe Val Asn Glu Asp Pro His						
	85			90		95
Ser Asn Val Phe Lys Ser Gly Phe Asn Leu Asp Pro His Glu Gln Asp						
	100		105		110	
Thr His Gln Gln Ala Gln Glu Glu Gln Gln His Thr Arg Glu Lys Thr						
	115		120		125	
Ser Thr Pro Pro Leu Pro Met His Phe Asn Ala Gln Arg Arg Thr Ser						
	130		135		140	
Val Ser Gly Glu Thr Leu Gln Pro Asn Asn Phe Asp Asp Trp Thr Pro						
	145		150		155	160
Asp His Tyr Lys Glu Lys Ser Glu Gln Gln Leu Gln Arg Leu Glu Lys						
		165		170		175
Ser Ile Arg Asn Asn Phe Leu Phe Asn Lys Leu Asp Ser Asp Ser Lys						
	180		185		190	
Arg Leu Val Ile Asn Cys Leu Glu Glu Lys Ser Val Pro Lys Gly Ala						
	195		200		205	
Thr Ile Ile Lys Gln Gly Asp Gln Gly Asp Tyr Phe Tyr Val Val Glu						
	210		215		220	
Lys Gly Thr Val Asp Phe Tyr Val Asn Asp Asn Lys Val Asn Ser Ser						
	225		230		235	240
Gly Pro Gly Ser Ser Phe Gly Glu Leu Ala Leu Met Tyr Asn Ser Pro						
		245		250		255
Arg Ala Ala Thr Val Val Ala Thr Ser Asp Cys Leu Leu Trp Ala Leu						
	260		265		270	
Asp Arg Leu Thr Phe Arg Lys Ile Leu Leu Gly Ser Ser Phe Lys Lys						
	275		280		285	
Arg Leu Met Tyr Asp Asp Leu Leu Lys Ser Met Pro Val Leu Lys Ser						
	290		295		300	

Leu Thr Thr Tyr Asp Arg Ala Lys Leu Ala Asp Ala Leu Asp Thr Lys
305 310 315 320

Ile Tyr Gln Pro Gly Glu Thr Ile Ile Arg Glu Gly Asp Gln Gly Glu
325 330 335

Asn Phe Tyr Leu Ile Glu Tyr Gly Ala Val Asp Val Ser Lys Lys Gly
340 345 350

Gln Gly Val Ile Asn Lys Leu Lys Asp His Asp Tyr Phe Gly Glu Val
355 360 365

Ala Leu Leu Asn Asp Leu Pro Arg Gln Ala Thr Val Thr Ala Thr Lys
370 375 380

Arg Thr Lys Val Ala Thr Leu Gly Lys Ser Gly Phe Gln Arg Leu Leu
385 390 395 400

Gly Pro Ala Val Asp Val Leu Lys Leu Asn Asp Pro Thr Arg His
405 410 415

<210> 41
<211> 412
<212> PRT
<213> Schizosaccharomyces pombe

<400> 41

Met Ser Phe Glu Glu Val Tyr Glu Glu Leu Lys Ala Leu Val Asp Glu
1 5 10 15

Gln Asn Pro Ser Asp Val Leu Gln Phe Cys Tyr Asp Phe Phe Gly Glu
20 25 30

Lys Leu Lys Ala Glu Arg Ser Val Phe Arg Arg Gly Asp Thr Ile Thr
35 40 45

Glu Ser Phe Ser Asp Gly Asp Glu Ser Asp Phe Leu Ser Glu Leu Asn
50 55 60

Asp Met Val Ala Gly Pro Glu Ala Ile Gly Pro Asp Ala Lys Tyr Val
65 70 75 80

Pro Glu Leu Gly Gly Leu Lys Glu Met Asn Val Ser Tyr Pro Gln Asn
85 90 95

Tyr Asn Leu Leu Arg Arg Gln Ser Val Ser Thr Glu Ser Met Asn Pro
 100 105 110

Ser Ala Phe Ala Leu Glu Thr Lys Arg Thr Phe Pro Pro Lys Asp Pro
 115 120 125

Glu Asp Leu Lys Arg Leu Lys Arg Ser Val Ala Gly Asn Phe Leu Phe
 130 135 140

Lys Asn Leu Asp Glu Glu His Tyr Asn Glu Val Leu Asn Ala Met Thr
 145 150 155 160

Glu Lys Arg Ile Gly Glu Ala Gly Val Ala Val Ile Val Gln Gly Ala
 165 170 175

Val Gly Asp Tyr Phe Tyr Ile Val Glu Gln Gly Glu Phe Asp Val Tyr
 180 185 190

Lys Arg Pro Glu Leu Asn Ile Thr Pro Glu Glu Val Leu Ser Ser Gly
 195 200 205

Tyr Gly Asn Tyr Ile Thr Thr Ile Ser Pro Gly Glu Tyr Phe Gly Glu
 210 215 220

Leu Ala Leu Met Tyr Asn Ala Pro Arg Ala Ala Ser Val Val Ser Lys
 225 230 235 240

Thr Pro Asn Asn Val Ile Tyr Ala Leu Asp Arg Thr Ser Phe Arg Arg
 245 250 255

Ile Val Phe Glu Asn Ala Tyr Arg Gln Arg Met Leu Tyr Glu Ser Leu
 260 265 270

Leu Glu Glu Val Pro Ile Leu Ser Ser Leu Asp Lys Tyr Gln Arg Gln
 275 280 285

Lys Ile Ala Asp Ala Leu Gln Thr Val Val Tyr Gln Ala Gly Ser Ile
 290 295 300

Val Ile Arg Gln Gly Asp Ile Gly Asn Gln Phe Tyr Leu Ile Glu Asp
 305 310 315 320

Thr Lys Gly Asp Tyr Phe Gly Glu Leu Ala Leu Ile His Glu Thr Val
340 345 350

Arg Asn Ala Thr Val Gln Ala Lys Thr Arg Leu Lys Leu Ala Thr Phe
355 360 365

Asp Lys Pro Thr Phe Asn Arg Leu Leu Gly Asn Ala Ile Asp Leu Met
370 375 380

Arg Asn Gln Pro Arg Ala Arg Met Gly Met Asp Asn Glu Tyr Gly Asp
385 390 395 400

Gln Ser Leu His Arg Ser Pro Pro Ser Thr Lys Ala
405 410

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<210> 42
<211> 248
<212> PRT
<213> Mucor rouxii
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<400> 42

Met Asp Glu Glu His Tyr Gln Asp Ile Val Asn Ala Met Ile Glu Lys
1 5 10 15

Pro Val Arg Lys Gly Glu Thr Ile Ile Glu Gln Gly Ala Val Gly Asp
20 25 30

Tyr Phe Tyr Val Val Ala Ser Gly Thr Phe Asp Cys Tyr Ile Lys Lys
35 40 45

Pro Gly Gln Glu Lys Pro Leu Lys Val Thr Ser Tyr Glu Arg Gly Gly
50 55 60

Ser Phe Gly Glu Leu Ala Leu Met Tyr Asn Ala Pro Arg Ala Ala Thr
65 70 75 80

Val Thr Ser Thr Ser Glu Ser Val Leu Trp Ala Leu Asp Arg Val Thr
85 90 95

Phe Arg Thr Ile Leu Met Glu Asn Thr Ala Leu Lys Arg Arg Val Tyr
100 105 110

Glu Ser Phe Leu Glu Glu Val Ala Leu Leu Ile Ser Leu Glu Pro Tyr
 115 120 125

Glu Arg His Lys Ile Ala Asp Ser Leu Glu Thr Ile Phe Phe Asn Asp
 130 135 140

Asn Gly His Val Ile Ser Gln Gly Asp Ile Gly Asp Gln Phe Tyr Ile
 145 150 155 160

Ile Glu Ser Gly Ser Ala Ile Val Tyr Lys Thr Asp Ser Asn Gly Asp
 165 170 175

Gln Gln Met Val Asn Gln Leu Glu Arg Gly Ala Tyr Phe Gly Glu Leu
 180 185 190

Ala Leu Leu Asn Asp Cys Pro Arg Ala Ala Thr Val Ile Ala Lys Gly
 195 200 205

Thr Leu Arg Cys Val Thr Leu Gly Lys Lys Ala Phe Thr Arg Leu Leu
 210 215 220

Gly Pro Val His Glu Ile Leu Lys Arg Asn Ala Glu Asn Tyr Gln Ala
 225 230 235 240

Ile Leu Ser Gln Gln Gln Gln Tyr
 245

<210> 43
 <211> 605
 <212> PRT
 <213> Mucor circinelloides

<400> 43

Met Ala Asp Phe Thr Asp Ser Leu Ile Lys Asn Ile Gly Val His Ser
 1 5 10 15

Ser Ser Pro Val Met Thr Ser Val Asn Met Gly Gln Leu Gly Glu Lys
 20 25 30

Leu Arg Gln Ala Arg Thr Thr Thr Leu Ala Ser Leu Ser Gln Ala Leu
 35 40 45

Ser Lys Lys Pro Glu Ala Ala Ala Ala Ala Ala Thr Ala Pro Asn Ala
 50 55 60

Val Asn Glu Ser Thr Thr Thr Pro Thr Thr Met Gln Leu Pro Ala Ser
65 70 75 80

Glu Lys Ala Thr Ser Gln Leu Glu Ile Asn Val Val Glu Ala Arg Asn
85 90 95

Leu Thr Ile Ala Asp Ala Arg Lys Ala Asp Thr Tyr Cys Ile Val His
100 105 110

Tyr Glu Gly Asn Thr Thr Ser Thr Leu Asp Lys Val Asp Asp Gly Ile
115 120 125

Leu Pro Ser Thr Pro Leu Val Ile Lys Ser Gln Val Ala Ser Gly Ala
130 135 140

Phe Lys Ala Phe Glu Ile Met Met Ser Ala Ser Ser Pro Lys Trp Met
145 150 155 160

His Arg Val Asn Phe Asp Val Thr Ala Gly Asn Lys Glu Ile Thr Val
165 170 175

Ser Val Tyr Asp Arg Gly Asn Lys Leu Pro Asn Gly Glu Asp Arg Phe
180 185 190

Leu Gly Met Ser Ser Ile Val Pro Asn Leu Val Asn Lys Lys Thr Val
195 200 205

Glu Leu Ile Phe Pro Leu His Gly Arg Pro Asp Asp Asp Gln Glu Val
210 215 220

Thr Gly Asp Val Arg Leu Gln Val Thr Phe Ile Asp Pro Lys Lys Ala
225 230 235 240

Asn Leu Lys Pro Glu Asp Phe Arg Ile Val Arg Met Ile Gly Gln Gly
245 250 255

Ser Val Gly Lys Val Tyr Glu Val Ile Lys Arg Asp Ser Gly Arg Thr
260 265 270

Tyr Ala Met Lys Val Leu Ser Lys Arg Leu Leu Leu Ala Glu Asn Glu
275 280 285

Val Asp Thr Ala Phe Asn Glu Arg Asn Val Leu Val Gln Ser Leu Ser
 290 295 300

Ser Pro Phe Ile Ala Asn Leu Lys Tyr Ser Phe Gln Thr Thr Asn His
 305 310 315 320

Leu Phe Leu Val Met Asp Tyr Phe Pro Gly Gly Glu Leu Phe Asp Phe
 325 330 335

Leu Glu Arg Glu Arg Cys Leu Ser Glu Lys Arg Cys Gln Phe Phe Ala
 340 345 350

Ala Glu Ile Val Cys Ala Phe Asp Asn Ile His Ala Arg Asn Ile Val
 355 360 365

Tyr Arg Asn Leu Lys Pro Glu Ser Ile Leu Leu Asp Ala His Gly His
 370 375 380

Ile Ala Leu Thr Asp Phe Gly Leu Cys Lys Gln Leu Lys Asn Lys Met
 385 390 395 400

Asp Leu Ile Gln Gly Val Pro Gln Val Ile Thr Gln Glu Tyr Leu Ala
 405 410 415

Pro Glu Met Val Met Gln Lys Pro Tyr Gly Met Ala Ala Asp Trp Trp
 420 425 430

Ser Leu Gly Val Leu Met Phe Glu Leu Leu Thr Gly Ser Pro Pro Phe
 435 440 445

His Ser Val Glu Gln Gly Glu Leu Phe Arg Gln Ile Leu Glu Ala Pro
 450 455 460

Ile Lys Phe Pro Ala Gly Gly Cys Ile Thr Glu Glu Ala Lys Asp Phe
 465 470 475 480

Ile Cys Gln Leu Leu Glu Arg Asp Pro Ala Lys Arg Leu Gly Ser His
 485 490 495

Gly Asp Val Ala Gln Val Lys Ala His Pro Phe Phe Lys Asp Leu Asn
 500 505 510

Trp Asp Val Val Tyr Lys Lys Gln Met Gln Leu Pro Phe Val Pro Glu
 515 520 525

Val Glu Glu Gln Leu Arg Glu Glu Ala Ile Ala Ala Ala Ala Ile
 530 535 540

Ser Ile Pro Val Thr Asn Ser Lys Thr Glu Ser Thr Asn Ala Asn Val
 545 550 555 560

Met Pro Val Ala Asp Gln Ser Lys Phe Lys Gly Phe Ser Tyr Ile Arg
 565 570 575

Glu Asp Val Met Ala Lys Lys Gly Glu His Arg Leu Gly Val Asn Pro
 580 585 590

Glu Asp Glu Asp Pro Glu Val Asp Phe Trp Phe Arg Gln
 595 600 605

<210> 44
 <211> 480
 <212> PRT
 <213> Aspergillus niger

<400> 44

Met Pro Ser Leu Gly Gly Leu Leu Lys Lys Arg Arg Thr Lys Asp Ser
 1 5 10 15

Gln Thr Leu Ser Lys Glu Leu Glu Ala Gly Ser Ala Gln Thr Gln Thr
 20 25 30

Ser Pro Asn Ala Ala Glu Asp His His Asn His Asn His His Gln His
 35 40 45

His His His Leu Phe His His His His Gln Pro Gln Pro Ala Thr Asn
 50 55 60

Ser Gly Ser Ala Ala Asn Thr Pro Pro Gln Pro Gln Asp Ser Val Pro
 65 70 75 80

Gln Gln Ser Asn Arg Ser Ser Gly Ala Glu Lys Ser Ser Asp Gly Gln
 85 90 95

Val Ala Ser Met Gln Ser Ala Val Thr Gln Ala Ser Pro Ser Ala His
 100 105 110

His Thr Ser Gly Leu Pro Gln Pro Asn Ala Asn Ala Ala Ser Ile Gln

115					120					125					
Asn	Ile	Ile	Asn	Pro	Ser	Gln	Gln	Gly	Ala	Met	His	Ser	Ala	Ser	Ser
130						135					140				
Gly	His	Thr	Gln	Ser	His	His	Ala	Gly	Arg	Ser	Asp	Ala	Arg	Thr	Thr
145					150					155					160
Lys	Gly	Lys	Tyr	Ser	Leu	Asp	Asp	Phe	Ser	Leu	Gln	Arg	Thr	Leu	Gly
				165					170					175	
Thr	Gly	Ser	Phe	Gly	Arg	Val	His	Leu	Val	Gln	Ser	Lys	His	Asn	His
			180					185					190		
Arg	Phe	Tyr	Ala	Val	Lys	Val	Leu	Lys	Lys	Ala	Gln	Val	Val	Lys	Met
		195					200					205			
Lys	Gln	Ile	Glu	His	Thr	Asn	Asp	Glu	Arg	Arg	Met	Leu	Asn	Arg	Val
	210					215					220				
Arg	His	Pro	Phe	Leu	Ile	Thr	Leu	Trp	Gly	Thr	Trp	Gln	Asp	Ser	Arg
225					230					235					240
Asn	Leu	Tyr	Met	Val	Met	Asp	Phe	Val	Glu	Gly	Gly	Glu	Leu	Phe	Ser
				245					250					255	
Leu	Val	Arg	Lys	Ser	Gln	Arg	Phe	Pro	Asn	Pro	Val	Ala	Lys	Phe	Tyr
			260					265					270		
Ala	Ala	Glu	Val	Thr	Leu	Ala	Leu	Glu	Tyr	Leu	His	Thr	Gln	Asn	Ile
		275				280					285				
Ile	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu	Leu	Leu	Asp	Arg	His	Gly
	290					295					300				
His	Leu	Lys	Ile	Thr	Asp	Phe	Gly	Phe	Ala	Lys	Glu	Val	Pro	Asp	Ile
305					310					315					320
Thr	Trp	Thr	Leu	Cys	Gly	Thr	Pro	Asp	Tyr	Leu	Ala	Pro	Glu	Val	Val
				325					330					335	
Ser	Ser	Lys	Gly	Tyr	Asn	Lys	Ser	Val	Asp	Trp	Trp	Ser	Leu	Gly	Ile
			340					345					350		

Leu Ile Phe Glu Met Leu Cys Gly Phe Thr Pro Phe Trp Asp Ser Gly
 355 360 365

Ser Pro Val Lys Ile Tyr Glu Asn Ile Leu Arg Gly Arg Val Lys Tyr
 370 375 380

Pro Pro Tyr Leu His Pro Asp Ala Val Asp Leu Leu Ser Gln Leu Ile
 385 390 395 400

Thr Ala Asp Leu Thr Lys Arg Leu Gly Asn Leu His Gly Gly Ser Asp
 405 410 415

Asp Val Lys Asn His Pro Trp Phe Ala Glu Val Thr Trp Asp Arg Leu
 420 425 430

Ala Arg Lys Asp Ile Asp Ala Pro Tyr Val Pro Pro Ile Arg Gly Gly
 435 440 445

Gln Gly Asp Ala Ser Gln Tyr Asp Arg Tyr Pro Glu Glu Thr Glu Gln
 450 455 460

Tyr Gly Met Ala Gly Glu Asp Pro His Gly His Leu Phe Pro Asp Phe
 465 470 475 480

<210> 45
 <211> 425
 <212> PRT
 <213> Blastocadiella emersonii

<400> 45

Met Thr Leu Ile Asp Lys Leu Met Glu Lys Thr Lys Lys Val Val Gly
 1 5 10 15

Ser Ser Asp Lys Asp Ala Pro Ala Pro Ala Ser Pro Ser Ser Pro Ser
 20 25 30

Thr Ala Ala Gly Ala Gly Ser Ala Ser Ser Thr Ala Ser Ser Thr Thr
 35 40 45

Thr Ala Ala Ala Ser Gly Asn Leu Ser Ile Pro Ser Pro Leu Val Ala
 50 55 60

Gly Ser Thr Thr Ser Ser Ser Ile Ser His Ala Gln Lys Met Ala Thr
 65 70 75 80

Ala Ala His Thr Asn Ser Asp Tyr Ser Pro Ser Pro Ala Ala Thr Pro
85 90 95

Ser Ala Pro Leu Asp Ala Val Ala Glu Arg Arg Arg Arg Lys Thr Thr
100 105 110

Leu Ala Asp Leu Glu Leu Arg Gln Thr Leu Gly Thr Gly Ser Phe Gly
115 120 125

Arg Val His Leu Val Arg Leu Arg Ser Thr Gly Lys Tyr Tyr Ala Met
130 135 140

Lys Val Leu Lys Lys Ala Glu Val Val Lys His Lys Gln Val Glu His
145 150 155 160

Thr Leu Asn Glu Lys Gly Ile Leu Glu Gln Ile Asp His Pro Phe Leu
165 170 175

Val Ala Leu His Ser Ser Phe Gln Asp Ser Ala Asn Leu Tyr Met Val
180 185 190

Met Glu Tyr Val Thr Gly Gly Glu Leu Phe Thr Tyr Leu Arg Arg Ser
195 200 205

Gln Arg Phe Ser Asn Asn Val Ala Lys Phe Tyr Ala Ala Glu Val Val
210 215 220

Leu Ala Phe Glu Tyr Leu His Ser Lys Asp Ile Ile Tyr Arg Asp Leu
225 230 235 240

Lys Pro Glu Asn Leu Leu Leu Asp Ala Gln Gly His Val Lys Ile Thr
245 250 255

Asp Phe Gly Phe Ala Lys His Val Pro Asp Ile Thr Trp Thr Leu Cys
260 265 270

Gly Thr Pro Asp Tyr Leu Ala Pro Glu Ile Ile Gln Ser Arg Gly Tyr
275 280 285

Gly Arg Ala Val Asp Trp Tyr Ala Leu Gly Val Leu Ile Phe Glu Met
290 295 300

Leu Ala Gly Tyr Pro Pro Phe Tyr Asp Glu Asp His Val Arg Met Tyr
305 310 315 320

Glu Lys Ile Leu Gln Gly Lys Val Lys Trp Pro Ser His Phe Asp Pro
325 330 335

Ala Ala Lys Asp Leu Leu Lys Arg Leu Leu Thr Thr Asp Leu Thr Lys
340 345 350

Arg Tyr Gly Asn Leu Lys Gly Gly Ser Lys Asp Ile Lys Met His Lys
355 360 365

Trp Phe Ala Gly Leu Asp Trp Thr Lys Leu Phe Asn Lys Gln Ile Pro
370 375 380

Pro Pro Tyr Thr Pro Pro Asn Arg Gly Asp Gly Asp Thr Ser Asn Phe
385 390 395 400

Asp Ala Tyr Pro Glu Glu Thr Glu Pro Tyr Gly Lys Val Gln Pro Asp
405 410 415

Pro Tyr Ala Gln Leu Phe Lys Asp Phe
420 425

<210> 46
<211> 442
<212> PRT
<213> Candida albicans

<400> 46

Met Val Asn Leu Leu Lys Lys Leu His Ile Thr Lys Ser His Gln Ser
1 5 10 15

Asn His Ser Asn Ser Asp Ser Asn Ser Leu Asn Ser Asn Thr Ser Met
20 25 30

Asp Asn His Gln Gln Gln Gln Gln Leu Gln Gln Tyr Gln Gln Gln Phe
35 40 45

Gln Gln Pro Gln Gln Gln Leu Tyr Pro Gly Glu Gln Ile Val His Pro
50 55 60

Ala Ala Ala Gln Thr Gly Gln Asn Thr Thr Asn Val Thr Ala Val Ser
65 70 75 80

Ser Ser Asn Ile Thr Gln Ser Ala Thr Ser Ser Leu His Ser Gln Gln
 85 90 95

Leu Gln His Val Asp Val Ser Lys Ser Ala Ala Glu Glu Ala Ile Arg
 100 105 110

Arg Ser Leu Leu Pro Glu Arg Ser Thr Val Ser Lys Gly Lys Tyr Ser
 115 120 125

Leu Thr Asp Phe Ser Ile Met Arg Thr Leu Gly Thr Gly Ser Phe Gly
 130 135 140

Arg Val His Leu Val Arg Ser Val His Asn Gly Arg Tyr Tyr Ala Ile
 145 150 155 160

Lys Val Leu Lys Lys His Gln Val Val Lys Met Lys Gln Val Glu His
 165 170 175

Thr Asn Asp Glu Arg Arg Met Leu Lys Leu Val Glu His Pro Phe Leu
 180 185 190

Ile Arg Met Trp Gly Thr Phe Gln Asp Ser Lys Asn Leu Phe Met Val
 195 200 205

Met Asp Tyr Ile Glu Gly Gly Glu Leu Phe Ser Leu Leu Arg Lys Ser
 210 215 220

Gln Arg Phe Pro Asn Pro Val Ala Lys Phe Tyr Ala Ala Glu Val Thr
 225 230 235 240

Leu Ala Leu Glu Tyr Leu His Ser His Asp Ile Ile Tyr Arg Asp Leu
 245 250 255

Lys Pro Glu Asn Ile Leu Leu Asp Arg Asn Gly His Ile Lys Ile Thr
 260 265 270

Asp Phe Gly Phe Ala Lys Glu Val Ser Thr Val Thr Trp Thr Leu Cys
 275 280 285

Gly Thr Pro Asp Tyr Ile Ala Pro Glu Val Ile Thr Thr Lys Pro Tyr
 290 295 300

Asn Lys Ser Val Asp Trp Trp Ser Leu Gly Val Leu Ile Phe Glu Met

305 310 315 320
 Leu Ala Gly Tyr Thr Pro Phe Tyr Asp Ser Thr Pro Met Lys Thr Tyr
 325 330 335
 Glu Lys Ile Leu Ala Gly Lys Ile His Tyr Pro Ser Phe Phe Gln Pro
 340 345 350
 Asp Val Ile Asp Leu Leu Thr Lys Leu Ile Thr Ala Asp Leu Thr Arg
 355 360 365
 Arg Leu Gly Asn Leu Ile Asn Gly Pro Ala Asp Ile Arg Asn His Pro
 370 375 380
 Trp Phe Ser Glu Val Val Trp Glu Lys Leu Leu Ala Lys Asp Ile Glu
 385 390 395 400
 Thr Pro Tyr Glu Pro Pro Ile Thr Ala Gly Val Gly Asp Ser Ser Leu
 405 410 415
 Phe Asp His Tyr Pro Glu Glu Gln Leu Asp Tyr Gly Ser Gln Gly Glu
 420 425 430
 Asp Pro Tyr Ala Ser Tyr Phe Leu Asp Phe
 435 440

 <210> 47
 <211> 380
 <212> PRT
 <213> *Saccharomyces cerevisiae*

 <400> 47
 Met Glu Phe Val Ala Glu Arg Ala Gln Pro Val Gly Gln Thr Ile Gln
 1 5 10 15
 Gln Gln Asn Val Asn Thr Tyr Gly Gln Gly Val Leu Gln Pro His His
 20 25 30
 Asp Leu Gln Gln Arg Gln Gln Gln Gln Gln Arg Gln His Gln Gln
 35 40 45
 Leu Leu Thr Ser Gln Leu Pro Gln Lys Ser Leu Val Ser Lys Gly Lys
 50 55 60

Tyr Thr Leu His Asp Phe Gln Ile Met Arg Thr Leu Gly Thr Gly Ser
65 70 75 80

Phe Gly Arg Val His Leu Val Arg Ser Val His Asn Gly Arg Tyr Tyr
85 90 95

Ala Ile Lys Val Leu Lys Lys Gln Gln Val Val Lys Met Lys Gln Val
100 105 110

Glu His Thr Asn Asp Glu Arg Arg Met Leu Lys Leu Val Glu His Pro
115 120 125

Phe Leu Ile Arg Met Trp Gly Thr Phe Gln Asp Ala Arg Asn Ile Phe
130 135 140

Met Val Met Asp Tyr Ile Glu Gly Gly Glu Leu Phe Ser Leu Leu Arg
145 150 155 160

Lys Ser Gln Arg Phe Pro Asn Pro Val Ala Lys Phe Tyr Ala Ala Glu
165 170 175

Val Ile Leu Ala Leu Glu Tyr Leu His Ala His Asn Ile Ile Tyr Arg
180 185 190

Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Arg Asn Gly His Ile Lys
195 200 205

Ile Thr Asp Phe Gly Phe Ala Lys Glu Val Gln Thr Val Thr Trp Thr
210 215 220

Leu Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu Val Ile Thr Thr Lys
225 230 235 240

Pro Tyr Asn Lys Ser Val Asp Trp Trp Ser Leu Gly Val Leu Ile Tyr
245 250 255

Glu Met Leu Ala Gly Tyr Thr Pro Phe Tyr Asp Thr Thr Pro Met Lys
260 265 270

Thr Tyr Glu Lys Ile Leu Gln Gly Lys Val Val Tyr Pro Pro Tyr Phe
275 280 285

His Pro Asp Val Val Asp Leu Leu Ser Lys Leu Ile Thr Ala Asp Leu
290 295 300

Thr Arg Arg Ile Gly Asn Leu Gln Ser Gly Ser Arg Asp Ile Lys Ala
305 310 315 320

His Pro Trp Phe Ser Glu Val Val Trp Glu Arg Leu Leu Ala Lys Asp
325 330 335

Ile Glu Thr Pro Tyr Glu Pro Pro Ile Thr Ser Gly Ile Gly Asp Thr
340 345 350

Ser Leu Phe Asp Gln Tyr Pro Glu Glu Gln Leu Asp Tyr Gly Ile Gln
355 360 365

Gly Asp Asp Pro Tyr Ala Glu Tyr Phe Gln Asp Phe
370 375 380

<210> 48
<211> 512
<212> PRT
<213> Schizosaccharomyces pombe

<400> 48

Met Asp Thr Thr Ala Val Ala Ser Lys Gly Ser Thr Asn Val Gly Ser
1 5 10 15

Ser Thr Asp Thr Leu Ser Thr Ser Ala Ser Leu His Pro Ser Met Asn
20 25 30

Ala Gly Ser Val Asn Glu Tyr Ser Glu Gln Gln Arg His Gly Thr Asn
35 40 45

Ser Phe Asn Gly Lys Pro Ser Val His Asp Ser Val Gly Ser Asp Ala
50 55 60

Ser Val Ser Asn Gly His Asn Asn His Asn Glu Ser Ser Leu Trp Thr
65 70 75 80

Ser Gly Ile Pro Lys Ala Leu Glu Glu Ala Thr Lys Ser Lys Lys Pro
85 90 95

Asp Ser Leu Val Ser Thr Ser Thr Ser Gly Cys Ala Ser Ala His Ser
100 105 110

Val Gly Tyr Gln Asn Ile Asp Asn Leu Ile Pro Ser Pro Leu Pro Glu

115	120	125
Ser Ala Ser Arg Ser Ser Ser Gln Ser Ser His Gln Arg His Ser Arg 130 135 140		
Asp Gly Arg Gly Glu Leu Gly Ser Glu His Gly Glu Arg Arg Ser Ala 145 150 155 160		
Met Asp Gly Leu Arg Asp Arg His Ile Arg Lys Val Arg Val Ser Gln 165 170 175		
Leu Leu Asp Leu Gln Arg Arg Arg Ile Arg Pro Ala Asp His Thr Thr 180 185 190		
Lys Asp Arg Tyr Gly Ile Gln Asp Phe Asn Phe Leu Gln Thr Leu Gly 195 200 205		
Thr Gly Ser Phe Gly Arg Val His Leu Val Gln Ser Asn His Asn Arg 210 215 220		
Leu Tyr Tyr Ala Ile Lys Val Leu Glu Lys Lys Lys Ile Val Asp Met 225 230 235 240		
Lys Gln Ile Glu His Thr Cys Asp Glu Arg Tyr Ile Leu Ser Arg Val 245 250 255		
Gln His Pro Phe Ile Thr Ile Leu Trp Gly Thr Phe Gln Asp Ala Lys 260 265 270		
Asn Leu Phe Met Val Met Asp Phe Ala Glu Gly Gly Glu Leu Phe Ser 275 280 285		
Leu Leu Arg Lys Cys His Arg Phe Pro Glu Lys Val Ala Lys Phe Tyr 290 295 300		
Ala Ala Glu Val Ile Leu Ala Leu Asp Tyr Leu His His Asn Gln Ile 305 310 315 320		
Val Tyr Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Asp Arg Phe Gly 325 330 335		
His Leu Lys Ile Val Asp Phe Gly Phe Ala Lys Arg Val Ser Thr Ser 340 345 350		

Asn Cys Cys Thr Leu Cys Gly Thr Pro Asp Tyr Leu Ala Pro Glu Ile
 355 360 365

Ile Ser Leu Lys Pro Tyr Asn Lys Ala Ala Asp Trp Trp Ser Leu Gly
 370 375 380

Ile Leu Ile Phe Glu Met Leu Ala Gly Tyr Pro Pro Phe Tyr Ser Glu
 385 390 395 400

Asn Pro Met Lys Leu Tyr Glu Asn Ile Leu Glu Gly Lys Val Asn Tyr
 405 410 415

Pro Ser Tyr Phe Ser Pro Ala Ser Ile Asp Leu Leu Ser His Leu Leu
 420 425 430

Gln Arg Asp Ile Thr Cys Arg Tyr Gly Asn Leu Lys Asp Gly Ser Met
 435 440 445

Asp Ile Ile Met His Pro Trp Phe Arg Asp Ile Ser Trp Asp Lys Ile
 450 455 460

Leu Thr Arg Lys Ile Glu Val Pro Tyr Val Pro Pro Ile Gln Ala Gly
 465 470 475 480

Met Gly Asp Ser Ser Gln Phe Asp Ala Tyr Ala Asp Val Ala Thr Asp
 485 490 495

Tyr Gly Thr Ser Glu Asp Pro Glu Phe Thr Ser Ile Phe Lys Asp Phe
 500 505 510

<210> 49

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 49

tttctctctt tcagggtttt tttcttcttc ttcatactat atctctatat attttataaa 60

tctcgagatg 70

<210> 50

<211> 125

<212> PRT

<213> Mucor circinelloides

<400> 50

Lys Phe Phe Leu Ala Thr Ala Pro Val Asn Trp Glu His Asn Lys Pro
1 5 10 15

Leu Lys Arg Phe Ala Leu Pro Gly Gly Ser Ala Ala Ala Ala Pro Gly
20 25 30

Gly Arg Ser Pro Asn Gly Ser Gly Glu Ser Ile Ser Cys Val Leu Trp
35 40 45

Asn Asp Leu Phe Phe Ile Thr Gly Thr Asp Ile Val Arg Ser Leu Thr
50 55 60

Phe Arg Phe His Ala Phe Gly Arg Pro Val Thr Asn Ala Lys Lys Phe
65 70 75 80

Glu Glu Gly Ile Phe Ser Asp Leu Arg Asn Leu Lys Pro Gly His Asp
85 90 95

Ala Arg Leu Glu Glu Pro Lys Ser Glu Leu Leu Asp Met Leu Tyr Lys
100 105 110

Asn Asn Cys Ile Arg Thr Gln Lys Lys Gln Lys Val Phe
115 120 125

<210> 51

<211> 111

<212> PRT

<213> Saccharomyces cerevisiae

<400> 51

Lys Phe Phe Leu Ala Thr Ala Pro Val Asn Trp Gln Glu Asn Gln Ile
1 5 10 15

Ile Arg Arg Tyr Tyr Leu Asn Ser Gly Gln Gly Phe Val Ser Cys Val
20 25 30

Phe Trp Asn Asn Leu Tyr Tyr Ile Thr Gly Thr Asp Ile Val Lys Cys
35 40 45

Cys Leu Tyr Arg Met Gln Lys Phe Gly Arg Glu Val Val Gln Lys Lys
50 55 60

Lys Phe Glu Glu Gly Ile Phe Ser Asp Leu Arg Asn Leu Lys Cys Gly
65 70 75 80

Ile Asp Ala Thr Leu Glu Gln Pro Lys Ser Glu Phe Leu Ser Phe Leu
85 90 95

Phe Arg Asn Met Cys Leu Lys Thr Gln Lys Lys Gln Lys Val Phe
100 105 110

<210> 52
<211> 111
<212> PRT
<213> Candida albicans

<400> 52

Lys Phe Phe Leu Ala Thr Ala Pro Ala Asn Trp Gln Glu Asn Gln Val
1 5 10 15

Ile Arg Arg Tyr Tyr Leu Asn His Asp Glu Gly Phe Val Ser Cys Val
20 25 30

Tyr Trp Asn Asn Leu Tyr Phe Ile Thr Gly Thr Asp Ile Val Arg Cys
35 40 45

Ile Val Tyr Lys Phe Glu His Phe Gly Arg Lys Ile Ile Asp Arg Lys
50 55 60

Lys Phe Glu Glu Gly Ile Phe Ser Asp Leu Arg Asn Leu Lys Cys Gly
65 70 75 80

Ala Asp Ala Ile Leu Glu Pro Pro Arg Ser Glu Phe Leu Glu Phe Leu
85 90 95

Phe Lys Asn Ser Cys Leu Arg Thr Gln Lys Lys Gln Lys Val Phe
100 105 110

<210> 53
<211> 111
<212> PRT
<213> Kluyveromyces lactis

<400> 53

Lys Phe Phe Leu Ala Thr Arg Pro Ala Asn Trp Gln Glu Asn Gln Val
1 5 10 15

Ile Arg Arg Tyr Tyr Leu Ser Asn Asp Glu Gly Phe Val Ser Cys Val
 20 25 30

Phe Trp Asn Asn Leu Tyr Tyr Ile Thr Gly Thr Asp Ile Val Arg Cys
 35 40 45

Cys Ala Tyr Arg Met Gln Lys Phe Gly Arg Glu Ile Val Glu Arg Lys
 50 55 60

Lys Phe Glu Glu Gly Ile Phe Ser Asp Leu Arg Asn Leu Lys Cys Gly
 65 70 75 80

Ile Asp Ala Thr Leu Glu Lys Pro Lys Ser Asp Leu Leu Ala Phe Leu
 85 90 95

Tyr Lys Asn Met Cys Leu Lys Thr Gln Lys Lys Gln Lys Val Phe
 100 105 110

<210> 54
 <211> 110
 <212> PRT
 <213> Aspergillus nidulans

<400> 54

Lys Tyr Phe Leu Leu Ser Ala Pro Val Asp Trp Gln Pro Asp Gln Leu
 1 5 10 15

Ile Arg Arg Phe Leu Leu Pro Thr Gly Asp Tyr Ile Ser Cys Val Leu
 20 25 30

Trp Ser Asn Leu Phe His Ile Ser Gly Thr Asp Ile Val Arg Cys Leu
 35 40 45

Ala Phe Arg Phe Gln Ala Phe Gly Arg Pro Val Lys Asn Ser Lys Lys
 50 55 60

Phe Glu Glu Gly Ile Phe Ser Asp Leu Arg Asn Leu Lys Ala Gly Thr
 65 70 75 80

Asp Ala Thr Leu Glu Glu Pro Lys Ser Pro Phe Leu Asp Phe Leu Tyr
 85 90 95

Lys Asn Asn Cys Ile Arg Thr Gln Lys Lys Gln Lys Val Phe
 100 105 110

<210> 55
 <211> 111
 <212> PRT
 <213> *Clavispora lusitaniae*

<400> 55

Lys Phe Phe Leu Ala Thr Ala Pro Ala Asn Trp Gln Glu Asn Gln Val
 1 5 10 15

Ile Arg Arg Tyr Tyr Leu Asn Asn Asp Glu Gly Phe Val Ser Cys Val
 20 25 30

Phe Trp Asn Asn Leu Tyr Phe Val Thr Gly Thr Asp Ile Val Arg Cys
 35 40 45

Ile Leu Tyr Lys Phe Gln His Phe Gly Arg Thr Ile Thr Asp Arg Lys
 50 55 60

Lys Phe Glu Glu Gly Ile Phe Ser Asp Leu Arg Asn Leu Lys Ala Gly
 65 70 75 80

Ser Asp Ser Val Leu Glu Glu Pro Lys Ser Pro Phe Leu Glu Phe Leu
 85 90 95

Tyr Asn Asn Ser Cys Leu Arg Thr Gln Lys Lys Gln Lys Val Phe
 100 105 110

<210> 56
 <211> 103
 <212> PRT
 <213> *Mucor circinelloides*

<400> 56

Tyr Ile Val Gln Glu Ile Met Glu Ala Asp Leu His Gln Ile Ile Arg
 1 5 10 15

Ser Gly Gln Pro Leu Thr Asp Ala His Phe Gln Tyr Phe Val Tyr Gln
 20 25 30

Ile Cys Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Leu His Arg
 35 40 45

Asp Leu Lys Pro Gly Lys Leu Arg Ile Asn Gly Ile Thr Gln Ile Thr
 50 55 60

Glu Pro Lys Ile Cys Asp Phe Gly Leu Ala Arg Gly Tyr Ser Glu Asn
65 70 75 80

Asp Glu His Asn Val Gly Phe Met Thr Glu Tyr Val Ala Thr Arg Trp
85 90 95

Tyr Arg Ala Pro Glu Ile Met
100

<210> 57
<211> 100
<212> PRT
<213> Schizosaccharomyces pombe

<400> 57

Tyr Ile Tyr Glu Glu Leu Met Glu Ala Asp Leu Asn Ala Ile Ile Lys
1 5 10 15

Ser Gly Gln Pro Leu Thr Asp Ala His Phe Gln Ser Phe Ile Tyr Gln
20 25 30

Ile Leu Cys Gly Leu Lys Tyr Ile His Ser Ala Asn Val Ile His Arg
35 40 45

Asp Leu Lys Pro Gly Asn Leu Leu Val Asn Ala Asp Cys Glu Leu Lys
50 55 60

Ile Cys Asp Phe Gly Leu Ala Arg Gly Cys Ser Glu Asn Pro Glu Glu
65 70 75 80

Asn Pro Gly Phe Met Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg Ala
85 90 95

Pro Glu Ile Met
100

<210> 58
<211> 100
<212> PRT
<213> Candida albicans

<400> 58

Tyr Leu Tyr Glu Glu Leu Met Glu Cys Asp Met His Gln Ile Ile Arg
1 5 10 15

Ser Gly Gln Pro Leu Ser Asp Gln His Tyr Gln Ser Phe Ile Tyr Gln
20 25 30

Val Leu Cys Gly Leu Asn Phe Ile His Ser Ala Asp Val Leu His Arg
35 40 45

Asp Leu Lys Pro Gly Asn Leu Leu Val Asn Ala Asp Cys Glu Leu Lys
50 55 60

Ile Cys Asp Phe Gly Leu Ala Arg Gly Phe Ser Glu Asn Pro Asp Glu
65 70 75 80

Asn Ala Gly Phe Met Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg Ala
85 90 95

Pro Glu Ile Met
100

<210> 59
<211> 98
<212> PRT
<213> Fusarium oxysporum

<400> 59

Tyr Leu Ile Gln Glu Leu Met Glu Thr Asp Met His Arg Val Ile Arg
1 5 10 15

Thr Gln Asp Leu Ser Asp Asp His Cys Gln Tyr Phe Ile Tyr Gln Thr
20 25 30

Leu Arg Ala Leu Lys Ala Met His Ser Ala Asn Val Leu His Arg Asp
35 40 45

Leu Lys Pro Ser Asn Leu Leu Leu Asn Ala Asn Cys Asp Leu Lys Val
50 55 60

Cys Asp Phe Gly Leu Ala Arg Ser Ala Ala Ser Gln Glu Asp Asn Ser
65 70 75 80

Gly Phe Met Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
85 90 95

Ile Met

<210> 60
 <211> 100
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 60

Tyr Leu Tyr Glu Glu Leu Met Glu Cys Asp Met His Gln Ile Ile Lys
 1 5 10 15

Ser Gly Gln Pro Leu Thr Asp Ala His Tyr Gln Ser Phe Thr Tyr Gln
 20 25 30

Ile Leu Cys Gly Leu Lys Tyr Ile His Ser Ala Asp Val Leu His Arg
 35 40 45

Asp Leu Lys Pro Gly Asn Leu Leu Val Asn Ala Asp Cys Gln Leu Lys
 50 55 60

Ile Cys Asp Phe Gly Leu Ala Arg Gly Tyr Ser Glu Asn Pro Val Glu
 65 70 75 80

Asn Ser Gln Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg Ala
 85 90 95

Pro Glu Ile Met
 100

<210> 61
 <211> 98
 <212> PRT
 <213> *Candida albicans*

<400> 61

Tyr Leu Ile Gln Glu Leu Met Glu Thr Asp Leu His Arg Val Ile Arg
 1 5 10 15

Thr Gln Asn Leu Ser Asp Asp His Ile Gln Tyr Phe Ile Tyr Gln Thr
 20 25 30

Leu Arg Ala Leu Lys Ala Met His Ser Ala Asn Val Leu His Arg Asp
 35 40 45

Leu Lys Pro Ser Asn Leu Leu Leu Asn Ser Asn Cys Asp Leu Lys Ile

50

55

60

Cys Asp Phe Gly Leu Ala Arg Ser Ile Ala Ser Gln Glu Asp Asn Tyr
 65 70 75 80

Gly Phe Met Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
 85 90 95

Ile Met

<210> 62
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> Xaa can be any amino acid

<220>
 <221> misc_feature
 <222> (5)..(6)
 <223> Xaa can be any amino acid

<220>
 <221> misc_feature
 <222> (8)..(8)
 <223> Xaa can be any amino acid

<220>
 <221> misc_feature
 <222> (10)..(11)
 <223> Xaa can be any amino acid

<400> 62

Ile Ser Xaa Pro Xaa Xaa Phe Xaa His Xaa Xaa His Val Gly
 1 5 10

<210> 63
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> Xaa can be any amino acid

<220>
 <221> misc_feature
 <222> (5)..(8)
 <223> Xaa can be any amino acid

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> Xaa can be any amino acid

<220>
 <221> misc_feature
 <222> (12)..(13)
 <223> Xaa can be any amino acid

<400> 63

Ile	Ser	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	His	Xaa	Xaa	His	Val	Gly
1			5					10						15	

<210> 64
 <211> 99
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<220>
 <221> misc_feature
 <222> (2)..(11)
 <223> Xaa can be any amino acid

<220>
 <221> misc_feature
 <222> (14)..(85)
 <223> Xaa can be any amino acid

<220>
 <221> misc_feature
 <222> (88)..(88)
 <223> Xaa can be any amino acid

<220>
 <221> misc_feature
 <222> (90)..(98)
 <223> Xaa can be any amino acid

<400> 64

Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Glu Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Xaa Xaa Cys

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Xaa Arg Asp Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Cys